

SEQUENCE LISTING

<110> Schopfer, Christel R.
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<120> Method for the production of Astaxanthin in flowers of plants

<130> 13173-00007-US

<150> PCT/EP2003/009102
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<150> DE 102 38 980.2
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<150> DE 102 38 978.0
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<150> DE 102 38 979.9
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<150> DE 102 53 112.9
 <151> 2002-11-13

<150> DE 102 58 971.2
 <151> 2002-12-16

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<170> PatentIn version 3.3

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<222> (166)..(1155)

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 Met Gln Leu Ala
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gcg aca gta atg ttg gag cag ctt acc gga agc gct gag gca ctc aag	225
Ala Thr Val Met Leu Glu Gln Leu Thr Gly Ser Ala Glu Ala Leu Lys	
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gag aag gag aag gag gtt gca ggc agc tct gac gtg ttg cgt aca tgg	273
Glu Lys Glu Lys Glu Val Ala Gly Ser Ser Asp Val Leu Arg Thr Trp	
25 30 35	
gcg acc cag tac tcg ctt ccg tca gaa gag tca gac gcg gcc cgc ccg	321
Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu Ser Asp Ala Ala Arg Pro	
40 45 50	
gga ctg aag aat gcc tac aag cca cca cct tcc gac aca aag ggc atc	369
Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser Asp Thr Lys Gly Ile	
55 60 65	
aca atg gcg cta cgt gtc atc ggc tcc tgg gcc gca gtg ttc ctc cac	417
Thr Met Ala Leu Arg Val Ile Gly Ser Trp Ala Val Phe Leu His	
70 75 80	
gcc att ttt caa atc aag ctt ccg acc tcc ttg gac cag ctg cac tgg	465
Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu Asp Gln Leu His Trp	
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ctg ccc gtg tca gat gcc aca gct cag ctg gtt agc ggc acg agc agc	513
Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val Ser Gly Thr Ser Ser	
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ctg ctc gac atc gtc gta gta ttc ttt gtc ctg gag ttc ctg tac aca	561
Leu Leu Asp Ile Val Val Val Phe Phe Val Leu Glu Phe Leu Tyr Thr	
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Gly Leu Phe Ile Thr Thr His Asp Ala Met His Gly Thr Ile Ala Met	
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aga aac agg cag ctt aat gac ttc ttg ggc aga gta tgc atc tcc ttg	657
Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg Val Cys Ile Ser Leu	
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tac gcc tgg ttt gat tac aac atg ctg cac cgc aag cat tgg gag cac	705
Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg Lys His Trp Glu His	
165 170 175 180	
cac aac cac act ggc gag gtg ggc aag gac cct gac ttc cac agg gga	753
His Asn His Thr Gly Glu Val Gly Lys Asp Pro Asp Phe His Arg Gly	
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Asn Pro Gly Ile Val Pro Trp Phe Ala Ser Phe Met Ser Ser Tyr Met	
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Ser Met Trp Gln Phe Ala Arg Leu Ala Trp Trp Thr Val Val Met Gln	
215 220 225	
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ccc atc ctg tcc gcc ttc cgc ttg ttc tac ttt ggc acg tac atg ccc			945
Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe Gly Thr Tyr Met Pro			
245	250	255	260
cac aag cct gag cct ggc gcc gcg tca ggc tct tca cca gcc gtc atg			993
His Lys Pro Glu Pro Gly Ala Ala Ser Gly Ser Ser Pro Ala Val Met			
	265	270	275
aac tgg tgg aag tcg cgc act agc cag gcg tcc gac ctg gtc agc ttt			1041
Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser Asp Leu Val Ser Phe			
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ctg acc tgc tac cac ttc gac ctg cac tgg gag cac cac cgc tgg ccc			1089
Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu His His Arg Trp Pro			
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Phe Ala Pro Trp Trp Glu Leu Pro Asn Cys Arg Arg Leu Ser Gly Arg			
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Gly Leu Val Pro Ala			
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<212> PRT

<213> Haematococcus pluvialis

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Leu Arg Thr Trp Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu Ser Asp
 35 40 45

Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser Asp
 50 55 60

Thr Lys Gly Ile Thr Met Ala Leu Arg Val Ile Gly Ser Trp Ala Ala
 65 70 75 80

Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu Asp
 85 90 95

Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val Ser
 100 105 110

Gly Thr Ser Ser Leu Leu Asp Ile Val Val Val Phe Phe Val Leu Glu
 115 120 125

Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala Met His Gly
 130 135 140

Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg Val
 145 150 155 160

Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg Lys
 165 170 175

His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys Asp Pro Asp
 180 185 190

Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala Ser Phe Met
 195 200 205

Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala Trp Trp Thr
 210 215 220

Val Val Met Gln Leu Leu Gly Ala Pro Met Ala Asn Leu Leu Val Phe
 225 230 235 240

Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe Gly
 245 250 255

Thr Tyr Met Pro His Lys Pro Glu Pro Gly Ala Ala Ser Gly Ser Ser
 260 265 270

Pro Ala Val Met Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser Asp
 275 280 285

Leu Val Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu His
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<212> DNA

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<222> (168)..(1130)

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ctccgtcctc tgccaaatct cgcgtcgggg cctgcctaag tcgaaga atg cac gtc	176
Met His Val	
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gca tcg gca cta atg gtc gag cag aaa ggc agt gag gca gct gct tcc	224
Ala Ser Ala Leu Met Val Glu Gln Lys Gly Ser Glu Ala Ala Ala Ser	
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agc cca gac gtc ttg aga gcg tgg gcg aca cag tat cac atg cca tcc	272
Ser Pro Asp Val Leu Arg Ala Trp Ala Thr Gln Tyr His Met Pro Ser	
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gag tcg tca gac gca gct cgt cct gcg cta aag cac gcc tac aaa cct	320
Glu Ser Ser Asp Ala Ala Arg Pro Ala Leu Lys His Ala Tyr Lys Pro	
40 45 50	
cca gca tct gac gcc aag ggc atc acg atg gcg ctg acc atc att ggc	368
Pro Ala Ser Asp Ala Lys Gly Ile Thr Met Ala Leu Thr Ile Ile Gly	

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aca tcc atg gac cag ctt cac tgg ttg cct gtg tcc gaa gcc aca gcc Thr Ser Met Asp Gln Leu His Trp Leu Pro Val Ser Glu Ala Thr Ala 85 90 95			464
cag ctt ttg ggc gga agc agc agc cta ctg cac atc gct gca gtc ttc Gln Leu Leu Gly Gly Ser Ser Ser Leu Leu His Ile Ala Ala Val Phe 100 105 110 115			512
att gta ctt gag ttc ctg tac act ggt cta ttc atc acc aca cat gac Ile Val Leu Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp 120 125 130			560
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gca ggc tct cag gtg atg gcc tgg ttc agg gcc aag aca agt gag gca Ala Gly Ser Gln Val Met Ala Trp Phe Arg Ala Lys Thr Ser Glu Ala 260 265 270 275			992
tct gat gtg atg agt ttc ctg aca tgc tac cac ttt gac ctg cac tgg Ser Asp Val Met Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp 280 285 290			1040
gag cac cac agg tgg ccc ttt gcc ccc tgg tgg cag ctg ccc cac tgc Glu His His Arg Trp Pro Phe Ala Pro Trp Trp Gln Leu Pro His Cys			1088

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<213> Haematococcus pluvialis

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Met Pro Ser Glu Ser Ser Asp Ala Ala Arg Pro Ala Leu Lys His Ala
35 40 45

Tyr Lys Pro Pro Ala Ser Asp Ala Lys Gly Ile Thr Met Ala Leu Thr
50 55 60

Ile Ile Gly Thr Trp Thr Ala Val Phe Leu His Ala Ile Phe Gln Ile
65 70 75 80

Arg Leu Pro Thr Ser Met Asp Gln Leu His Trp Leu Pro Val Ser Glu
85 90 95

Ala Thr Ala Gln Leu Leu Gly Gly Ser Ser Ser Leu Leu His Ile Ala

100	105	110
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Thr His Asp Ala Met His Gly Thr Ile Ala Leu Arg His Arg Gln Leu 130	135	140
Asn Asp Leu Leu Gly Asn Ile Cys Ile Ser Leu Tyr Ala Trp Phe Asp 145	150	155
Tyr Ser Met Leu His Arg Lys His Trp Glu His His Asn His Thr Gly 165	170	175
Glu Val Gly Lys Asp Pro Asp Phe His Lys Gly Asn Pro Gly Leu Val 180	185	190
Pro Trp Phe Ala Ser Phe Met Ser Ser Tyr Met Ser Leu Trp Gln Phe 195	200	205
Ala Arg Leu Ala Trp Trp Ala Val Val Met Gln Met Leu Gly Ala Pro 210	215	220
Met Ala Asn Leu Leu Val Phe Met Ala Ala Ala Pro Ile Leu Ser Ala 225	230	235
Phe Arg Leu Phe Tyr Phe Gly Thr Tyr Leu Pro His Lys Pro Glu Pro 245	250	255
Gly Pro Ala Ala Gly Ser Gln Val Met Ala Trp Phe Arg Ala Lys Thr 260	265	270
Ser Glu Ala Ser Asp Val Met Ser Phe Leu Thr Cys Tyr His Phe Asp 275	280	285
Leu His Trp Glu His His Arg Trp Pro Phe Ala Pro Trp Trp Gln Leu 290	295	300
Pro His Cys Arg Arg Leu Ser Gly Arg Gly Leu Val Pro Ala Leu Ala 305	310	315
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Ile Val Ser Gly Gly Ile Ile Ala Ala Trp Leu Ala Leu His Val His	
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gcg ctg tgg ttt ctg gac gca gcg gcg cat ccc atc ctg gcg atc gca	144
Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Ile Ala	
35 40 45	
aat ttc ctg ggg ctg acc tgg ctg tcg gtc gga ttg ttc atc atc gcg	192
Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala	
50 55 60	
cat gac gcg atg cac ggg tcg gtg gtg ccg ggg cgt ccg cgc gcc aat	240
His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn	
65 70 75 80	
gcg gcg atg ggc cag ctt gtc ctg tgg ctg tat gcc gga ttt tcg tgg	288
Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp	
85 90 95	
cgc aag atg atc gtc aag cac atg gcc cat cac cgc cat gcc gga acc	336
Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr	
100 105 110	
gac gac gac ccc gat ttc gac cat ggc ggc ccg gtc cgc tgg tac gcc	384
Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala	
115 120 125	
cgc ttc atc ggc acc tat ttc ggc tgg cgc gag ggg ctg ctg ctg ccc	432
Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro	
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gtc atc gtg acg gtc tat gcg ctg atc ctt ggg gat cgc tgg atg tac	480
Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr	
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gtg gtc ttc tgg ccg ctg ccg tcg atc ctg gcg tcg atc cag ctg ttc	528
Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe	
165 170 175	
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Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro	
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Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu	
195 200 205	

ctg acc tgc ttt cac ttt ggc ggt tat cat cac gaa cac cac ctg cac 672
 Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His
 210 215 220

ccg acg gtg ccg tgg tgg cgc ctg ccc agc acc cgc acc aag ggg gac 720
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 225 230 235 240

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 Thr Ala

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<212> PRT

<213> Agrobacterium aurantiacum

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 20 25 30

Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Ile Ala
 35 40 45

Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala
 50 55 60

His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn
 65 70 75 80

Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp
 85 90 95

Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr
 100 105 110

Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala
 115 120 125

Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro
 130 135 140

Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr
 145 150 155 160

Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe
 165 170 175

Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro
 180 185 190

Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu
 195 200 205

Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His
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Thr Ala

<210> 7

<211> 1631

<212> DNA

<213> Alcaligenes sp.

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<222> (99)..(827)

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 Met Ser Gly Arg Lys Pro
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ggc aca act ggc gac acg atc gtc aat ctc ggt ctg acc gcc gcg atc 164
 Gly Thr Thr Gly Asp Thr Ile Val Asn Leu Gly Leu Thr Ala Ala Ile
 10 15 20

ctg ctg tgc tgg ctg gtc ctg cac gcc ttt acg cta tgg ttg cta gat 212
 Leu Leu Cys Trp Leu Val Leu His Ala Phe Thr Leu Trp Leu Leu Asp
 25 30 35

gcg gcc gcg cat ccg ctg ctt gcc gtg ctg tgc ctg gct ggg ctg acc 260
 Ala Ala Ala His Pro Leu Leu Ala Val Leu Cys Leu Ala Gly Leu Thr
 40 45 50

tgg ctg tcg gtc ggg ctg ttc atc atc gcg cat gac gca atg cac ggg Trp Leu Ser Val Gly Leu Phe Ile Ile Ala His Asp Ala Met His Gly 55 60 65 70	308
tcc gtg gtg ccg ggg cgg ccg cgc gcc aat gcg gcg atc ggg caa ctg Ser Val Val Pro Gly Arg Pro Arg Ala Asn Ala Ala Ile Gly Gln Leu 75 80 85	356
gcg ctg tgg ctc tat gcg ggg ttc tcg tgg ccc aag ctg atc gcc aag Ala Leu Trp Leu Tyr Ala Gly Phe Ser Trp Pro Lys Leu Ile Ala Lys 90 95 100	404
cac atg acg cat cac cgg cac gcc ggc acc gac aac gat ccc gat ttc His Met Thr His His Arg His Ala Gly Thr Asp Asn Asp Pro Asp Phe 105 110 115	452
ggt cac gga ggg ccc gtg cgc tgg tac ggc agc ttc gtc tcc acc tat Gly His Gly Gly Pro Val Arg Trp Tyr Gly Ser Phe Val Ser Thr Tyr 120 125 130	500
ttc ggc tgg cga gag gga ctg ctg cta ccg gtg atc gtc acc acc tat Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro Val Ile Val Thr Thr Tyr 135 140 145 150	548
gcg ctg atc ctg ggc gat cgc tgg atg tat gtc atc ttc tgg ccg gtc Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr Val Ile Phe Trp Pro Val 155 160 165	596
ccg gcc gtt ctg gcg tcg atc cag att ttc gtc ttc gga act tgg ctg Pro Ala Val Leu Ala Ser Ile Gln Ile Phe Val Phe Gly Thr Trp Leu 170 175 180	644
ccc cac cgc ccg gga cat gac gat ttt ccc gac cgg cac aac gcg agg Pro His Arg Pro Gly His Asp Asp Phe Pro Asp Arg His Asn Ala Arg 185 190 195	692
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<210> 8

<211> 242

<212> PRT

<213> *Alcaligenes* sp.

<400> 8

Met Ser Gly Arg Lys Pro Gly Thr Thr Gly Asp Thr Ile Val Asn Leu
 1 5 10 15

Gly Leu Thr Ala Ala Ile Leu Leu Cys Trp Leu Val Leu His Ala Phe
 20 25 30

Thr Leu Trp Leu Leu Asp Ala Ala Ala His Pro Leu Leu Ala Val Leu
 35 40 45

Cys Leu Ala Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala
 50 55 60

His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn
 65 70 75 80

Ala Ala Ile Gly Gln Leu Ala Leu Trp Leu Tyr Ala Gly Phe Ser Trp
 85 90 95

Pro Lys Leu Ile Ala Lys His Met Thr His His Arg His Ala Gly Thr
 100 105 110

Asp Asn Asp Pro Asp Phe Gly His Gly Gly Pro Val Arg Trp Tyr Gly
 115 120 125

Ser Phe Val Ser Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro
 130 135 140

Val Ile Val Thr Thr Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr
 145 150 155 160

Val Ile Phe Trp Pro Val Pro Ala Val Leu Ala Ser Ile Gln Ile Phe
 165 170 175

Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Asp Phe Pro
 180 185 190

Asp Arg His Asn Ala Arg Ser Thr Gly Ile Gly Asp Pro Leu Ser Leu
 195 200 205

Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His
 210 215 220

Pro His Val Pro Trp Trp Arg Leu Pro Arg Thr Arg Lys Thr Gly Gly
 225 230 235 240

Arg Ala

<210> 9

<211> 729*

<212> DNA

<213> *Paracoccus marcusii*

<220>

<221> CDS

<222> (1)..(729)

<400> 9

atg agc gca cat gcc ctg ccc aag gca gat ctg acc gcc aca agc ctg	48
Met Ser Ala His Ala Leu Pro Lys Ala Asp Leu Thr Ala Thr Ser Leu	
1 5 10 15	
atc gtc tcg ggc ggc atc atc gcc gca tgg ctg gcc ctg cat gtg cat	96
Ile Val Ser Gly Gly Ile Ile Ala Ala Trp Leu Ala Leu His Val His	
20 25 30	
gcg ctg tgg ttt ctg gac gcg gcg gcc cat ccc atc ctg gcg gtc gcg	144
Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Val Ala	
35 40 45	

aat ttc ctg ggg ctg acc tgg ctg tcg gtc gga ttg ttc atc atc gcg Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala 50 55 60	192
cat gac gcg atg cac ggg tcg gtc gtg ccg ggg cgt ccg cgc gcc aat His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn 65 70 75 80	240
gcg gcg atg ggc cag ctt gtc ctg tgg ctg tat gcc gga ttt tcg tgg Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp 85 90 95	288
cgc aag atg atc gtc aag cac atg gcc cat cac cgc cat gcc gga acc Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr 100 105 110	336
gac gac gac cca gat ttc gac cat ggc ggc ccg gtc cgc tgg tac gcc Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala 115 120 125	384
cgc ttc atc ggc acc tat ttc ggc tgg cgc gag ggg ctg ctg ctg ccc Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro 130 135 140	432
gtc atc gtg acg gtc tat gcg ctg atc ctg ggg gat cgc tgg atg tac Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr 145 150 155 160	480
gtg gtc ttc tgg ccg ttg ccg tcg atc ctg gcg tcg atc cag ctg ttc Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe 165 170 175	528
gtg ttc ggc act tgg ctg ccg cac cgc ccc ggc cac gac gcg ttc ccg Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro 180 185 190	576
gac cgc cat aat gcg cgg tcg tcg cgg atc agc gac cct gtg tcg ctg Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu 195 200 205	624
ctg acc tgc ttt cat ttt ggc ggt tat cat cac gaa cac cac ctg cac Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His 210 215 220	672
ccg acg gtg ccg tgg tgg cgc ctg ccc agc acc cgc acc aag ggg gac Pro Thr Val Pro Trp Trp Arg Leu Pro Ser Thr Arg Thr Lys Gly Asp 225 230 235 240	720
acc gca tga Thr Ala	729

<210> 10

<211> 242

<212> PRT

<213> Paracoccus marcusii

<400> 10

Met Ser Ala His Ala Leu Pro Lys Ala Asp Leu Thr Ala Thr Ser Leu
 1 5 10 15

Ile Val Ser Gly Gly Ile Ile Ala Ala Trp Leu Ala Leu His Val His
 20 25 30

Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Val Ala
 35 40 45

Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala
 50 55 60

His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn
 65 70 75 80

Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp
 85 90 95

Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr
 100 105 110

Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala
 115 120 125

Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro
 130 135 140

Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr
 145 150 155 160

Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe
 165 170 175

Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro
 180 185 190

Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu
 195 200 205

Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His
 210 215 220

Pro Thr Val Pro Trp Trp Arg Leu Pro Ser Thr Arg Thr Lys Gly Asp

225

230

235

240

Thr Ala

<210> 11

<211> 1629

<212> DNA

<213> Synechococystis

<220>

<221> CDS

<400> 11

atg atc acc acc gat gtt gtc att att ggg gcg ggg cac aat ggc tta	48
Met Ile Thr Thr Asp Val Val Ile Ile Gly Ala Gly His Asn Gly Leu	
1 5 10 15	
gtc tgt gca gcc tat ttg ctc caa cgg ggc ttg ggg gtg acg tta cta	96
Val Cys Ala Ala Tyr Leu Leu Gln Arg Gly Leu Gly Val Thr Leu Leu	
20 25 30	
gaa aag cgg gaa gta cca ggg ggg gcg gcc acc aca gaa gct ctc atg	144
Glu Lys Arg Glu Val Pro Gly Gly Ala Ala Thr Thr Glu Ala Leu Met	
35 40 45	
ccg gag cta tcc ccc cag ttt cgc ttt aac cgc tgt gcc att gac cac	192
Pro Glu Leu Ser Pro Gln Phe Arg Phe Asn Arg Cys Ala Ile Asp His	
50 55 60	
gaa ttt atc ttt ctg ggg ccg gtg ttg cag gag cta aat tta gcc cag	240
Glu Phe Ile Phe Leu Gly Pro Val Leu Gln Glu Leu Asn Leu Ala Gln	
65 70 75 80	
tat ggt ttg gaa tat tta ttt tgt gac ccc agt gtt ttt tgt ccg ggg	288
Tyr Gly Leu Glu Tyr Leu Phe Cys Asp Pro Ser Val Phe Cys Pro Gly	
85 90 95	
ctg gat ggc caa gct ttt atg agc tac cgt tcc cta gaa aaa acc tgt	336
Leu Asp Gly Gln Ala Phe Met Ser Tyr Arg Ser Leu Glu Lys Thr Cys	
100 105 110	
gcc cac att gcc acc tat agc ccc cga gat gcg gaa aaa tat cgg caa	384
Ala His Ile Ala Thr Tyr Ser Pro Arg Asp Ala Glu Lys Tyr Arg Gln	
115 120 125	
ttt gtc aat tat tgg acg gat ttg ctc aac gct gtc cag cct gct ttt	432
Phe Val Asn Tyr Trp Thr Asp Leu Leu Asn Ala Val Gln Pro Ala Phe	
130 135 140	
aat gct ccg ccc cag gct tta cta gat tta gcc ctg aac tat ggt tgg	480
Asn Ala Pro Pro Gln Ala Leu Leu Asp Leu Ala Leu Asn Tyr Gly Trp	
145 150 155 160	

gaa aac tta aaa tcc gtg ctg gcg atc gcc ggg tcg aaa acc aag gcg Glu Asn Leu Lys Ser Val Leu Ala Ile Ala Gly Ser Lys Thr Lys Ala 165 170 175	528
ttg gat ttt atc cgc act atg atc ggc tcc ccg gaa gat gtg ctc aat Leu Asp Phe Ile Arg Thr Met Ile Gly Ser Pro Glu Asp Val Leu Asn 180 185 190	576
gaa tgg ttc gac agc gaa cgg gtt aaa gct cct tta gct aga cta tgt Glu Trp Phe Asp Ser Glu Arg Val Lys Ala Pro Leu Ala Arg Leu Cys 195 200 205	624
tcg gaa att ggc gct ccc cca tcc caa aag ggt agt agc tcc ggc atg Ser Glu Ile Gly Ala Pro Pro Ser Gln Lys Gly Ser Ser Ser Gly Met 210 215 220	672
atg atg gtg gcc atg cgg cat ttg gag gga att gcc aga cca aaa gga Met Met Val Ala Met Arg His Leu Glu Gly Ile Ala Arg Pro Lys Gly 225 230 235 240	720
ggc act gga gcc ctc aca gaa gcc ttg gtg aag tta gtg caa gcc caa Gly Thr Gly Ala Leu Thr Glu Ala Leu Val Lys Leu Val Gln Ala Gln 245 250 255	768
ggg gga aaa atc ctc act gac caa acc gtc aaa cgg gta ttg gtg gaa Gly Gly Lys Ile Leu Thr Asp Gln Thr Val Lys Arg Val Leu Val Glu 260 265 270	816
aac aac cag gcg atc ggg gtg gag gta gct aac gga gaa cag tac cgg Asn Asn Gln Ala Ile Gly Val Glu Val Ala Asn Gly Glu Gln Tyr Arg 275 280 285	864
gcc aaa aaa ggc gtg att tct aac atc gat gcc cgc cgt tta ttt ttg Ala Lys Lys Gly Val Ile Ser Asn Ile Asp Ala Arg Arg Leu Phe Leu 290 295 300	912
caa ttg gtg gaa ccg ggg gcc cta gcc aag gtg aat caa aac cta ggg Gln Leu Val Glu Pro Gly Ala Leu Ala Lys Val Asn Gln Asn Leu Gly 305 310 315 320	960
gaa cga ctg gaa cgg cgc act gtg aac aat aac gaa gcc att tta aaa Glu Arg Leu Glu Arg Arg Thr Val Asn Asn Asn Glu Ala Ile Leu Lys 325 330 335	1008
atc gat tgt gcc ctc tcc ggt tta ccc cac ttc act gcc atg gcc ggg Ile Asp Cys Ala Leu Ser Gly Leu Pro His Phe Thr Ala Met Ala Gly 340 345 350	1056
ccg gag gat cta acg gga act att ttg att gcc gac tcg gta cgc cat Pro Glu Asp Leu Thr Gly Thr Ile Leu Ile Ala Asp Ser Val Arg His 355 360 365	1104
gtc gag gaa gcc cac gcc ctc att gcc ttg ggg caa att ccc gat gct Val Glu Glu Ala His Ala Leu Ile Ala Leu Gly Gln Ile Pro Asp Ala 370 375 380	1152
aat ccg tct tta tat ttg gat att ccc act gta ttg gac ccc acc atg Asn Pro Ser Leu Tyr Leu Asp Ile Pro Thr Val Leu Asp Pro Thr Met 385 390 395 400	1200

gcc ccc cct ggg cag cac acc ctc tgg atc gaa ttt ttt gcc ccc tac 1248
 Ala Pro Pro Gly Gln His Thr Leu Trp Ile Glu Phe Phe Ala Pro Tyr
 405 410 415

cgc atc gcc ggg ttg gaa ggg aca ggg tta atg ggc aca ggt tgg acc 1296
 Arg Ile Ala Gly Leu Glu Gly Thr Gly Leu Met Gly Thr Gly Trp Thr
 420 425 430

gat gag tta aag gaa aaa gtg gcg gat cgg gtg att gat aaa tta acg 1344
 Asp Glu Leu Lys Glu Lys Val Ala Asp Arg Val Ile Asp Lys Leu Thr
 435 440 445

gac tat gcc cct aac cta aaa tct ctg atc att ggt cgc cga gtg gaa 1392
 Asp Tyr Ala Pro Asn Leu Lys Ser Leu Ile Ile Gly Arg Arg Val Glu
 450 455 460

agt ccc gcc gaa ctg gcc caa cgg ctg gga agt tac aac ggc aat gtc 1440
 Ser Pro Ala Glu Leu Ala Gln Arg Leu Gly Ser Tyr Asn Gly Asn Val
 465 470 475 480

tat cat ctg gat atg agt ttg gac caa atg atg ttc ctc cgg cct cta 1488
 Tyr His Leu Asp Met Ser Leu Asp Gln Met Met Phe Leu Arg Pro Leu
 485 490 495

ccg gaa att gcc aac tac caa acc ccc atc aaa aat ctt tac tta aca 1536
 Pro Glu Ile Ala Asn Tyr Gln Thr Pro Ile Lys Asn Leu Tyr Leu Thr
 500 505 510

ggg gcg ggt acc cat ccc ggt ggc tcc ata tca ggt atg ccc ggt aga 1584
 Gly Ala Gly Thr His Pro Gly Gly Ser Ile Ser Gly Met Pro Gly Arg
 515 520 525

aat tgc gct cgg gtc ttt tta aaa caa caa cgt cgt ttt tgg taa 1629
 Asn Cys Ala Arg Val Phe Leu Lys Gln Gln Arg Arg Phe Trp
 530 535 540

<210> 12

<211> 542

<212> PRT

<213> Synechococystis

<400> 12

Met Ile Thr Thr Asp Val Val Ile Ile Gly Ala Gly His Asn Gly Leu
1 5 10 15

Val Cys Ala Ala Tyr Leu Leu Gln Arg Gly Leu Gly Val Thr Leu Leu
20 25 30

Glu Lys Arg Glu Val Pro Gly Gly Ala Ala Thr Thr Glu Ala Leu Met
35 40 45

Pro Glu Leu Ser Pro Gln Phe Arg Phe Asn Arg Cys Ala Ile Asp His

50

55

60

Glu Phe Ile Phe Leu Gly Pro Val Leu Gln Glu Leu Asn Leu Ala Gln
65 70 75 80

Tyr Gly Leu Glu Tyr Leu Phe Cys Asp Pro Ser Val Phe Cys Pro Gly
85 90 95

Leu Asp Gly Gln Ala Phe Met Ser Tyr Arg Ser Leu Glu Lys Thr Cys
100 105 110

Ala His Ile Ala Thr Tyr Ser Pro Arg Asp Ala Glu Lys Tyr Arg Gln
115 120 125

Phe Val Asn Tyr Trp Thr Asp Leu Leu Asn Ala Val Gln Pro Ala Phe
130 135 140

Asn Ala Pro Pro Gln Ala Leu Leu Asp Leu Ala Leu Asn Tyr Gly Trp
145 150 155 160

Glu Asn Leu Lys Ser Val Leu Ala Ile Ala Gly Ser Lys Thr Lys Ala
165 170 175

Leu Asp Phe Ile Arg Thr Met Ile Gly Ser Pro Glu Asp Val Leu Asn
180 185 190

Glu Trp Phe Asp Ser Glu Arg Val Lys Ala Pro Leu Ala Arg Leu Cys
195 200 205

Ser Glu Ile Gly Ala Pro Pro Ser Gln Lys Gly Ser Ser Ser Gly Met
210 215 220

Met Met Val Ala Met Arg His Leu Glu Gly Ile Ala Arg Pro Lys Gly
225 230 235 240

Gly Thr Gly Ala Leu Thr Glu Ala Leu Val Lys Leu Val Gln Ala Gln
245 250 255

Gly Gly Lys Ile Leu Thr Asp Gln Thr Val Lys Arg Val Leu Val Glu
260 265 270

Asn Asn Gln Ala Ile Gly Val Glu Val Ala Asn Gly Glu Gln Tyr Arg
275 280 285

Ala Lys Lys Gly Val Ile Ser Asn Ile Asp Ala Arg Arg Leu Phe Leu

290

295

300

Gln Leu Val Glu Pro Gly Ala Leu Ala Lys Val Asn Gln Asn Leu Gly
 305 310 315 320

Glu Arg Leu Glu Arg Arg Thr Val Asn Asn Asn Glu Ala Ile Leu Lys
 325 330 335

Ile Asp Cys Ala Leu Ser Gly Leu Pro His Phe Thr Ala Met Ala Gly
 340 345 350

Pro Glu Asp Leu Thr Gly Thr Ile Leu Ile Ala Asp Ser Val Arg His
 355 360 365

Val Glu Glu Ala His Ala Leu Ile Ala Leu Gly Gln Ile Pro Asp Ala
 370 375 380

Asn Pro Ser Leu Tyr Leu Asp Ile Pro Thr Val Leu Asp Pro Thr Met
 385 390 395 400

Ala Pro Pro Gly Gln His Thr Leu Trp Ile Glu Phe Phe Ala Pro Tyr
 405 410 415

Arg Ile Ala Gly Leu Glu Gly Thr Gly Leu Met Gly Thr Gly Trp Thr
 420 425 430

Asp Glu Leu Lys Glu Lys Val Ala Asp Arg Val Ile Asp Lys Leu Thr
 435 440 445

Asp Tyr Ala Pro Asn Leu Lys Ser Leu Ile Ile Gly Arg Arg Val Glu
 450 455 460

Ser Pro Ala Glu Leu Ala Gln Arg Leu Gly Ser Tyr Asn Gly Asn Val
 465 470 475 480

Tyr His Leu Asp Met Ser Leu Asp Gln Met Met Phe Leu Arg Pro Leu
 485 490 495

Pro Glu Ile Ala Asn Tyr Gln Thr Pro Ile Lys Asn Leu Tyr Leu Thr
 500 505 510

Gly Ala Gly Thr His Pro Gly Gly Ser Ile Ser Gly Met Pro Gly Arg
 515 520 525

Asn Cys Ala Arg Val Phe Leu Lys Gln Gln Arg Arg Phe Trp

530

535

540

<210> 13

<211> 776

<212> DNA

<213> Bradyrhizobium sp.

<220>

<221> CDS

<222> (1)..(774)

<400> 13

atg	cat	gca	gca	acc	gcc	aag	gct	act	gag	ttc	ggg	gcc	tct	cgg	cgc	48
Met	His	Ala	Ala	Thr	Ala	Lys	Ala	Thr	Glu	Phe	Gly	Ala	Ser	Arg	Arg	
1				5					10					15		

gac	gat	gcg	agg	cag	cgc	cgc	gtc	ggg	ctc	acg	ctg	gcc	gcg	gtc	atc	96
Asp	Asp	Ala	Arg	Gln	Arg	Arg	Val	Gly	Leu	Thr	Leu	Ala	Ala	Val	Ile	
			20					25					30			

atc	gcc	gcc	tgg	ctg	gtg	ctg	cat	gtc	ggg	ctg	atg	ttc	ttc	tgg	ccg	144
Ile	Ala	Ala	Trp	Leu	Val	Leu	His	Val	Gly	Leu	Met	Phe	Phe	Trp	Pro	
		35					40					45				

ctg	acc	ctt	cac	agc	ctg	ctg	ccg	gct	ttg	cct	ctg	gtg	gtg	ctg	cag	192
Leu	Thr	Leu	His	Ser	Leu	Leu	Pro	Ala	Leu	Pro	Leu	Val	Val	Leu	Gln	
	50					55					60					

acc	tgg	ctc	tat	gta	ggc	ctg	ttc	atc	atc	gcg	cat	gac	tgc	atg	cac	240
Thr	Trp	Leu	Tyr	Val	Gly	Leu	Phe	Ile	Ile	Ala	His	Asp	Cys	Met	His	
65					70					75					80	

ggc	tcg	ctg	gtg	ccg	ttc	aag	ccg	cag	gtc	aac	cgc	cgt	atc	gga	cag	288
Gly	Ser	Leu	Val	Pro	Phe	Lys	Pro	Gln	Val	Asn	Arg	Arg	Ile	Gly	Gln	
				85					90					95		

ctc	tgc	ctg	ttc	ctc	tat	gcc	ggg	ttc	tcc	ttc	gac	gct	ctc	aat	gtc	336
Leu	Cys	Leu	Phe	Leu	Tyr	Ala	Gly	Phe	Ser	Phe	Asp	Ala	Leu	Asn	Val	
			100					105						110		

gag	cac	cac	aag	cat	cac	cgc	cat	ccc	ggc	acg	gcc	gag	gat	ccc	gat	384
Glu	His	His	Lys	His	His	Arg	His	Pro	Gly	Thr	Ala	Glu	Asp	Pro	Asp	
		115					120					125				

ttc	gac	gag	gtg	ccg	ccg	cac	ggc	ttc	tgg	cac	tgg	ttc	gcc	agc	ttt	432
Phe	Asp	Glu	Val	Pro	Pro	His	Gly	Phe	Trp	His	Trp	Phe	Ala	Ser	Phe	
	130					135					140					

ttc	ctg	cac	tat	ttc	ggc	tgg	aag	cag	gtc	gcg	atc	atc	gca	gcc	gtc	480
Phe	Leu	His	Tyr	Phe	Gly	Trp	Lys	Gln	Val	Ala	Ile	Ile	Ala	Ala	Val	
145					150					155					160	

tcg ctg gtt tat cag ctc gtc ttc gcc gtt ccc ttg cag aac atc ctg 528
 Ser Leu Val Tyr Gln Leu Val Phe Ala Val Pro Leu Gln Asn Ile Leu
 165 170 175

ctg ttc tgg gcg ctg ccc ggg ctg ctg tcg gcg ctg cag ctg ttc acc 576
 Leu Phe Trp Ala Leu Pro Gly Leu Leu Ser Ala Leu Gln Leu Phe Thr
 180 185 190

ttc ggc acc tat ctg ccg cac aag ccg gcc acg cag ccc ttc gcc gat 624
 Phe Gly Thr Tyr Leu Pro His Lys Pro Ala Thr Gln Pro Phe Ala Asp
 195 200 205

cgc cac aac gcg cgg acg agc gaa ttt ccc gcg tgg ctg tcg ctg ctg 672
 Arg His Asn Ala Arg Thr Ser Glu Phe Pro Ala Trp Leu Ser Leu Leu
 210 215 220

acc tgc ttc cac ttc ggc ttt cat cac gag cat cat ctg cat ccc gat 720
 Thr Cys Phe His Phe Gly Phe His His Glu His His Leu His Pro Asp
 225 230 235 240

gcg ccg tgg tgg cgg ctg ccg gag atc aag cgg cgg gcc ctg gaa agg 768
 Ala Pro Trp Trp Arg Leu Pro Glu Ile Lys Arg Arg Ala Leu Glu Arg
 245 250 255

cgt gac ta 776
 Arg Asp

<210> 14

<211> 258

<212> PRT

<213> Bradyrhizobium sp.

<400> 14

Met His Ala Ala Thr Ala Lys Ala Thr Glu Phe Gly Ala Ser Arg Arg
 1 5 10 15

Asp Asp Ala Arg Gln Arg Arg Val Gly Leu Thr Leu Ala Ala Val Ile
 20 25 30

Ile Ala Ala Trp Leu Val Leu His Val Gly Leu Met Phe Phe Trp Pro
 35 40 45

Leu Thr Leu His Ser Leu Leu Pro Ala Leu Pro Leu Val Val Leu Gln
 50 55 60

Thr Trp Leu Tyr Val Gly Leu Phe Ile Ile Ala His Asp Cys Met His
 65 70 75 80

Gly Ser Leu Val Pro Phe Lys Pro Gln Val Asn Arg Arg Ile Gly Gln
 85 90 95

Leu Cys Leu Phe Leu Tyr Ala Gly Phe Ser Phe Asp Ala Leu Asn Val
 100 105 110

Glu His His Lys His His Arg His Pro Gly Thr Ala Glu Asp Pro Asp
 115 120 125

Phe Asp Glu Val Pro Pro His Gly Phe Trp His Trp Phe Ala Ser Phe
 130 135 140

Phe Leu His Tyr Phe Gly Trp Lys Gln Val Ala Ile Ile Ala Ala Val
 145 150 155 160

Ser Leu Val Tyr Gln Leu Val Phe Ala Val Pro Leu Gln Asn Ile Leu
 165 170 175

Leu Phe Trp Ala Leu Pro Gly Leu Leu Ser Ala Leu Gln Leu Phe Thr
 180 185 190

Phe Gly Thr Tyr Leu Pro His Lys Pro Ala Thr Gln Pro Phe Ala Asp
 195 200 205

Arg His Asn Ala Arg Thr Ser Glu Phe Pro Ala Trp Leu Ser Leu Leu
 210 215 220

Thr Cys Phe His Phe Gly Phe His His Glu His His Leu His Pro Asp
 225 230 235 240

Ala Pro Trp Trp Arg Leu Pro Glu Ile Lys Arg Arg Ala Leu Glu Arg
 245 250 255

Arg Asp

<210> 15

<211> 777

<212> DNA

<213> Nostoc sp.

<220>

<221> CDS

<400> 15
 atg gtt cag tgt caa cca tca tct ctg cat tca gaa aaa ctg gtg tta 48
 Met Val Gln Cys Gln Pro Ser Ser Leu His Ser Glu Lys Leu Val Leu
 1 5 10 15

ttg tca tcg aca atc aga gat gat aaa aat att aat aag ggt ata ttt 96
 Leu Ser Ser Thr Ile Arg Asp Asp Lys Asn Ile Asn Lys Gly Ile Phe
 20 25 30

att gcc tgc ttt atc tta ttt tta tgg gca att agt tta atc tta tta 144
 Ile Ala Cys Phe Ile Leu Phe Leu Trp Ala Ile Ser Leu Ile Leu Leu
 35 40 45

ctc tca ata gat aca tcc ata att cat aag agc tta tta ggt ata gcc 192
 Leu Ser Ile Asp Thr Ser Ile Ile His Lys Ser Leu Leu Gly Ile Ala
 50 55 60

atg ctt tgg cag acc ttc tta tat aca ggt tta ttt att act gct cat 240
 Met Leu Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His
 65 70 75 80

gat gcc atg cac ggc gta gtt tat ccc aaa aat ccc aga ata aat aat 288
 Asp Ala Met His Gly Val Val Tyr Pro Lys Asn Pro Arg Ile Asn Asn
 85 90 95

ttt ata ggt aag ctc act cta atc ttg tat gga cta ctc cct tat aaa 336
 Phe Ile Gly Lys Leu Thr Leu Ile Leu Tyr Gly Leu Leu Pro Tyr Lys
 100 105 110

gat tta ttg aaa aaa cat tgg tta cac cac gga cat cct ggt act gat 384
 Asp Leu Leu Lys Lys His Trp Leu His His Gly His Pro Gly Thr Asp
 115 120 125

tta gac cct gat tat tac aat ggt cat ccc caa aat ttc ttt ctt tgg 432
 Leu Asp Pro Asp Tyr Tyr Asn Gly His Pro Gln Asn Phe Phe Leu Trp
 130 135 140

tat cta cat ttt atg aag tct tat tgg cga tgg acg caa att ttc gga 480
 Tyr Leu His Phe Met Lys Ser Tyr Trp Arg Trp Thr Gln Ile Phe Gly
 145 150 155 160

tta gtg atg att ttt cat gga ctt aaa aat ctg gtg cat ata cca gaa 528
 Leu Val Met Ile Phe His Gly Leu Lys Asn Leu Val His Ile Pro Glu
 165 170 175

aat aat tta att ata ttt tgg atg ata cct tct att tta agt tca gta 576
 Asn Asn Leu Ile Ile Phe Trp Met Ile Pro Ser Ile Leu Ser Ser Val
 180 185 190

caa cta ttt tat ttt ggt aca ttt ttg cct cat aaa aag cta gaa ggt 624
 Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Lys Lys Leu Glu Gly
 195 200 205

ggg tat act aac ccc cat tgt gcg cgc agt atc cca tta cct ctt ttt 672
 Gly Tyr Thr Asn Pro His Cys Ala Arg Ser Ile Pro Leu Pro Leu Phe
 210 215 220

tgg tct ttt gtt act tgt tat cac ttc ggc tac cac aag gaa cat cac 720
 Trp Ser Phe Val Thr Cys Tyr His Phe Gly Tyr His Lys Glu His His

225 230 235 240

gaa tac cct caa ctt cct tgg tgg aaa tta cct gaa gct cac aaa ata 768
 Glu Tyr Pro Gln Leu Pro Trp Trp Lys Leu Pro Glu Ala His Lys Ile
 245 250 255

tct tta taa 777
 Ser Leu

<210> 16

<211> 258

<212> PRT

<213> Nostoc sp.

<400> 16

Met Val Gln Cys Gln Pro Ser Ser Leu His Ser Glu Lys Leu Val Leu
 1 5 10 15

Leu Ser Ser Thr Ile Arg Asp Asp Lys Asn Ile Asn Lys Gly Ile Phe
 20 25 30

Ile Ala Cys Phe Ile Leu Phe Leu Trp Ala Ile Ser Leu Ile Leu Leu
 35 40 45

Leu Ser Ile Asp Thr Ser Ile Ile His Lys Ser Leu Leu Gly Ile Ala
 50 55 60

Met Leu Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His
 65 70 75 80

Asp Ala Met His Gly Val Val Tyr Pro Lys Asn Pro Arg Ile Asn Asn
 85 90 95

Phe Ile Gly Lys Leu Thr Leu Ile Leu Tyr Gly Leu Leu Pro Tyr Lys
 100 105 110

Asp Leu Leu Lys Lys His Trp Leu His His Gly His Pro Gly Thr Asp
 115 120 125

Leu Asp Pro Asp Tyr Tyr Asn Gly His Pro Gln Asn Phe Phe Leu Trp
 130 135 140

Tyr Leu His Phe Met Lys Ser Tyr Trp Arg Trp Thr Gln Ile Phe Gly
 145 150 155 160

Leu Val Met Ile Phe His Gly Leu Lys Asn Leu Val His Ile Pro Glu
 165 170 175

Asn Asn Leu Ile Ile Phe Trp Met Ile Pro Ser Ile Leu Ser Ser Val
 180 185 190

Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Lys Lys Leu Glu Gly
 195 200 205

Gly Tyr Thr Asn Pro His Cys Ala Arg Ser Ile Pro Leu Pro Leu Phe
 210 215 220

Trp Ser Phe Val Thr Cys Tyr His Phe Gly Tyr His Lys Glu His His
 225 230 235 240

Glu Tyr Pro Gln Leu Pro Trp Trp Lys Leu Pro Glu Ala His Lys Ile
 245 250 255

Ser Leu

<210> 17

<211> 1608

<212> DNA

<213> Haematococcus pluvialis

<220>

<221> CDS

<222> (3)..(971)

<400> 17

ct aca ttt cac aag ccc gtg agc ggt gca agc gct ctg ccc cac atc 47
 Thr Phe His Lys Pro Val Ser Gly Ala Ser Ala Leu Pro His Ile
 1 5 10 15

ggc cca cct cct cat ctc cat cgg tca ttt gct gct acc acg atg ctg 95
 Gly Pro Pro Pro His Leu His Arg Ser Phe Ala Ala Thr Thr Met Leu
 20 25 30

tcg aag ctg cag tca atc agc gtc aag gcc cgc cgc gtt gaa cta gcc 143
 Ser Lys Leu Gln Ser Ile Ser Val Lys Ala Arg Arg Val Glu Leu Ala
 35 40 45

cgc gac atc acg cgg ccc aaa gtc tgc ctg cat gct cag cgg tgc tcg 191
 Arg Asp Ile Thr Arg Pro Lys Val Cys Leu His Ala Gln Arg Cys Ser
 50 55 60

tta gtt cgg ctg cga gtg gca gca cca cag aca gag gag gcg ctg gga Leu Val Arg Leu Arg Val Ala Ala Pro Gln Thr Glu Glu Ala Leu Gly 65 70 75	239
acc gtg cag gct gcc ggc gcg ggc gat gag cac agc gcc gat gta gca Thr Val Gln Ala Ala Gly Ala Gly Asp Glu His Ser Ala Asp Val Ala 80 85 90 95	287
ctc cag cag ctt gac cgg gct atc gca gag cgt cgt gcc cgg cgc aaa Leu Gln Gln Leu Asp Arg Ala Ile Ala Glu Arg Arg Ala Arg Arg Lys 100 105 110	335
cgg gag cag ctg tca tac cag gct gcc gcc att gca gca tca att ggc Arg Glu Gln Leu Ser Tyr Gln Ala Ala Ala Ile Ala Ala Ser Ile Gly 115 120 125	383
gtg tca ggc att gcc atc ttc gcc acc tac ctg aga ttt gcc atg cac Val Ser Gly Ile Ala Ile Phe Ala Thr Tyr Leu Arg Phe Ala Met His 130 135 140	431
atg acc gtg ggc ggc gca gtg cca tgg ggt gaa gtg gct ggc act ctc Met Thr Val Gly Gly Ala Val Pro Trp Gly Glu Val Ala Gly Thr Leu 145 150 155	479
ctc ttg gtg gtt ggt ggc gcg ctc ggc atg gag atg tat gcc cgc tat Leu Leu Val Val Gly Gly Ala Leu Gly Met Glu Met Tyr Ala Arg Tyr 160 165 170 175	527
gca cac aaa gcc atc tgg cat gag tcg cct ctg ggc tgg ctg ctg cac Ala His Lys Ala Ile Trp His Glu Ser Pro Leu Gly Trp Leu Leu His 180 185 190	575
aag agc cac cac aca cct cgc act gga ccc ttt gaa gcc aac gac ttg Lys Ser His His Thr Pro Arg Thr Gly Pro Phe Glu Ala Asn Asp Leu 195 200 205	623
ttt gca atc atc aat gga ctg ccc gcc atg ctc ctg tgt acc ttt ggc Phe Ala Ile Ile Asn Gly Leu Pro Ala Met Leu Leu Cys Thr Phe Gly 210 215 220	671
ttc tgg ctg ccc aac gtc ctg ggg gcg gcc tgc ttt gga gcg ggg ctg Phe Trp Leu Pro Asn Val Leu Gly Ala Ala Cys Phe Gly Ala Gly Leu 225 230 235	719
ggc atc acg cta tac ggc atg gca tat atg ttt gta cac gat ggc ctg Gly Ile Thr Leu Tyr Gly Met Ala Tyr Met Phe Val His Asp Gly Leu 240 245 250 255	767
gtg cac agg cgc ttt ccc acc ggg ccc atc gct ggc ctg ccc tac atg Val His Arg Arg Phe Pro Thr Gly Pro Ile Ala Gly Leu Pro Tyr Met 260 265 270	815
aag cgc ctg aca gtg gcc cac cag cta cac cac agc ggc aag tac ggt Lys Arg Leu Thr Val Ala His Gln Leu His His Ser Gly Lys Tyr Gly 275 280 285	863
ggc gcg ccc tgg ggt atg ttc ttg ggt cca cag gag ctg cag cac att Gly Ala Pro Trp Gly Met Phe Leu Gly Pro Gln Glu Leu Gln His Ile 290 295 300	911

cca ggt gcg gcg gag gag gtg gag cga ctg gtc ctg gaa ctg gac tgg 959
 Pro Gly Ala Ala Glu Glu Val Glu Arg Leu Val Leu Glu Leu Asp Trp
 305 310 315

tcc aag cgg tag ggtgcggaac caggcacgct ggtttcacac ctcatgcctg 1011
 Ser Lys Arg
 320

tgataagggtg tggctagagc gatgcgtgtg agacgggtat gtcacgggtcg actggtctga 1071

tggccaatgg catcgcccat gtctgggtcat cacgggctgg ttgcctgggt gaagggtgatg 1131

cacatcatca tgtgcggttg gaggggctgg cacagtgtgg gctgaactgg agcagttgtc 1191

caggctggcg ttgaatcagt gagggtttgt gattggcgggt tgtgaagcaa tgactccgcc 1251

catattctat ttgtgggagc tgagatgatg gcatgcttgg gatgtgcatg gatcatggta 1311

gtgcagcaaa ctatattcac ctagggctgt tggtaggatc aggtgaggcc ttgcacattg 1371

catgatgtac tcgtcatggt gtgttggtga gaggatggat gtggatggat gtgtattctc 1431

agacgtagac cttgactgga ggcttgatcg agagagtggg ccgtattctt tgagagggga 1491

ggctcgtgcc agaaatggtg agtggatgac tgtgacgctg tacattgcag gcaggtgaga 1551

tgcactgtct cgattgtaaa atacattcag atgcaaaaaa aaaaaaaaaa aaaaaaa 1608

<210> 18

<211> 322

<212> PRT

<213> Haematococcus pluvialis

<400> 18

Thr Phe His Lys Pro Val Ser Gly Ala Ser Ala Leu Pro His Ile Gly
 1 5 10 15

Pro Pro Pro His Leu His Arg Ser Phe Ala Ala Thr Thr Met Leu Ser
 20 25 30

Lys Leu Gln Ser Ile Ser Val Lys Ala Arg Arg Val Glu Leu Ala Arg
 35 40 45

Asp Ile Thr Arg Pro Lys Val Cys Leu His Ala Gln Arg Cys Ser Leu
 50 55 60

Val Arg Leu Arg Val Ala Ala Pro Gln Thr Glu Glu Ala Leu Gly Thr
 65 70 75 80

Val Gln Ala Ala Gly Ala Gly Asp Glu His Ser Ala Asp Val Ala Leu
85 90 95

Gln Gln Leu Asp Arg Ala Ile Ala Glu Arg Arg Ala Arg Arg Lys Arg
100 105 110

Glu Gln Leu Ser Tyr Gln Ala Ala Ala Ile Ala Ala Ser Ile Gly Val
115 120 125

Ser Gly Ile Ala Ile Phe Ala Thr Tyr Leu Arg Phe Ala Met His Met
130 135 140

Thr Val Gly Gly Ala Val Pro Trp Gly Glu Val Ala Gly Thr Leu Leu
145 150 155 160

Leu Val Val Gly Gly Ala Leu Gly Met Glu Met Tyr Ala Arg Tyr Ala
165 170 175

His Lys Ala Ile Trp His Glu Ser Pro Leu Gly Trp Leu Leu His Lys
180 185 190

Ser His His Thr Pro Arg Thr Gly Pro Phe Glu Ala Asn Asp Leu Phe
195 200 205

Ala Ile Ile Asn Gly Leu Pro Ala Met Leu Leu Cys Thr Phe Gly Phe
210 215 220

Trp Leu Pro Asn Val Leu Gly Ala Ala Cys Phe Gly Ala Gly Leu Gly
225 230 235 240

Ile Thr Leu Tyr Gly Met Ala Tyr Met Phe Val His Asp Gly Leu Val
245 250 255

His Arg Arg Phe Pro Thr Gly Pro Ile Ala Gly Leu Pro Tyr Met Lys
260 265 270

Arg Leu Thr Val Ala His Gln Leu His His Ser Gly Lys Tyr Gly Gly
275 280 285

Ala Pro Trp Gly Met Phe Leu Gly Pro Gln Glu Leu Gln His Ile Pro
290 295 300

Gly Ala Ala Glu Glu Val Glu Arg Leu Val Leu Glu Leu Asp Trp Ser
305 310 315 320

Lys Arg

<210> 19

<211> 1503

<212> DNA

<213> Tomato

<220>

<221> CDS

<400> 19

atg gat act ttg ttg aaa acc cca aat aac ctt gaa ttt ctg aac cca	48
Met Asp Thr Leu Leu Lys Thr Pro Asn Asn Leu Glu Phe Leu Asn Pro	
1 5 10 15	
cat cat ggt ttt gct gtt aaa gct agt acc ttt aga tct gag aag cat	96
His His Gly Phe Ala Val Lys Ala Ser Thr Phe Arg Ser Glu Lys His	
20 25 30	
cat aat ttt ggt tct agg aag ttt tgt gaa act ttg ggt aga agt gtt	144
His Asn Phe Gly Ser Arg Lys Phe Cys Glu Thr Leu Gly Arg Ser Val	
35 40 45	
tgt gtt aag ggt agt agt agt gct ctt tta gag ctt gta cct gag acc	192
Cys Val Lys Gly Ser Ser Ser Ala Leu Leu Glu Leu Val Pro Glu Thr	
50 55 60	
aaa aag gag aat ctt gat ttt gag ctt cct atg tat gac cct tca aaa	240
Lys Lys Glu Asn Leu Asp Phe Glu Leu Pro Met Tyr Asp Pro Ser Lys	
65 70 75 80	
ggg gtt gtt gtg gat ctt gct gtg gtt ggt ggt ggc cct gca gga ctt	288
Gly Val Val Val Asp Leu Ala Val Val Gly Gly Gly Pro Ala Gly Leu	
85 90 95	
gct gtt gca cag caa gtt tct gaa gca gga ctc tct gtt tgt tca att	336
Ala Val Ala Gln Gln Val Ser Glu Ala Gly Leu Ser Val Cys Ser Ile	
100 105 110	
gat ccg aat cct aaa ttg ata tgg cct aat aac tat ggt gtt tgg gtg	384
Asp Pro Asn Pro Lys Leu Ile Trp Pro Asn Asn Tyr Gly Val Trp Val	
115 120 125	
gat gaa ttt gag gct atg gac ttg tta gat tgt cta gat gct acc tgg	432
Asp Glu Phe Glu Ala Met Asp Leu Leu Asp Cys Leu Asp Ala Thr Trp	
130 135 140	
tct ggt gca gca gtg tac att gat gat aat acg gct aaa gat ctt cat	480
Ser Gly Ala Ala Val Tyr Ile Asp Asp Asn Thr Ala Lys Asp Leu His	
145 150 155 160	
aga cct tat gga agg gtt aac cgg aaa cag ctg aaa tcg aaa atg atg	528
Arg Pro Tyr Gly Arg Val Asn Arg Lys Gln Leu Lys Ser Lys Met Met	
165 170 175	

cag aaa tgt ata atg aat ggt gtt aaa ttc cac caa gcc aaa gtt ata Gln Lys Cys Ile Met Asn Gly Val Lys Phe His Gln Ala Lys Val Ile 180 185 190	576
aag gtg att cat gag gaa tcg aaa tcc atg ttg ata tgc aat gat ggt Lys Val Ile His Glu Glu Ser Lys Ser Met Leu Ile Cys Asn Asp Gly 195 200 205	624
att act att cag gca acg gtg gtg ctc gat gca act ggc ttc tct aga Ile Thr Ile Gln Ala Thr Val Val Leu Asp Ala Thr Gly Phe Ser Arg 210 215 220	672
tct ctt gtt cag tat gat aag cct tat aac ccc ggg tat caa gtt gct Ser Leu Val Gln Tyr Asp Lys Pro Tyr Asn Pro Gly Tyr Gln Val Ala 225 230 235 240	720
tat ggc att ttg gct gaa gtg gaa gag cac ccc ttt gat gta aac aag Tyr Gly Ile Leu Ala Glu Val Glu Glu His Pro Phe Asp Val Asn Lys 245 250 255	768
atg gtt ttc atg gat tgg cga gat tct cat ttg aag aac aat act gat Met Val Phe Met Asp Trp Arg Asp Ser His Leu Lys Asn Asn Thr Asp 260 265 270	816
ctc aag gag aga aat agt aga ata cca act ttt ctt tat gca atg cca Leu Lys Glu Arg Asn Ser Arg Ile Pro Thr Phe Leu Tyr Ala Met Pro 275 280 285	864
ttt tca tcc aac agg ata ttt ctt gaa gaa aca tca ctc gta gct cgt Phe Ser Ser Asn Arg Ile Phe Leu Glu Glu Thr Ser Leu Val Ala Arg 290 295 300	912
cct ggc ttg cgt ata gat gat att caa gaa cga atg gtg gct cgt tta Pro Gly Leu Arg Ile Asp Asp Ile Gln Glu Arg Met Val Ala Arg Leu 305 310 315 320	960
aac cat ttg ggg ata aaa gtg aag agc att gaa gaa gat gaa cat tgt Asn His Leu Gly Ile Lys Val Lys Ser Ile Glu Glu Asp Glu His Cys 325 330 335	1008
cta ata cca atg ggt ggt cca ctt cca gta tta cct cag aga gtc gtt Leu Ile Pro Met Gly Gly Pro Leu Pro Val Leu Pro Gln Arg Val Val 340 345 350	1056
gga atc ggt ggt aca gct ggc atg gtt cat cca tcc acc ggt tat atg Gly Ile Gly Gly Thr Ala Gly Met Val His Pro Ser Thr Gly Tyr Met 355 360 365	1104
gtg gca agg aca cta gct gcg gct cct gtt gtt gcc aat gcc ata att Val Ala Arg Thr Leu Ala Ala Pro Val Val Ala Asn Ala Ile Ile 370 375 380	1152
caa tac ctc ggt tct gaa aga agt cat tcg ggt aat gaa tta tcc aca Gln Tyr Leu Gly Ser Glu Arg Ser His Ser Gly Asn Glu Leu Ser Thr 385 390 395 400	1200
gct gtt tgg aaa gat ttg tgg cct ata gag agg aga cgt caa aga gag Ala Val Trp Lys Asp Leu Trp Pro Ile Glu Arg Arg Arg Gln Arg Glu 405 410 415	1248

ttc ttc tgc ttc ggt atg gat att ctt ctg aag ctt gat tta cct gct 1296
Phe Phe Cys Phe Gly Met Asp Ile Leu Leu Lys Leu Asp Leu Pro Ala
420 425 430

aca aga agg ttc ttt gat gca ttc ttt gac tta gaa cct cgt tat tgg 1344
Thr Arg Arg Phe Phe Asp Ala Phe Phe Asp Leu Glu Pro Arg Tyr Trp
435 440 445

cat ggc ttc tta tcg tct cga ttg ttt cta cct gaa ctc ata gtt ttt 1392
His Gly Phe Leu Ser Ser Arg Leu Phe Leu Pro Glu Leu Ile Val Phe
450 455 460

ggg ctg tct cta ttc tct cat gct tca aat act tct aga ttt gag ata 1440
Gly Leu Ser Leu Phe Ser His Ala Ser Asn Thr Ser Arg Phe Glu Ile
465 470 475 480

atg aca aag gga act gtt cca tta gta aat atg atc aac aat ttg tta 1488
Met Thr Lys Gly Thr Val Pro Leu Val Asn Met Ile Asn Asn Leu Leu
485 490 495

cag gat aaa gaa tga 1503
Gln Asp Lys Glu
500

<210> 20

<211> 500

<212> PRT

<213> Tomato

<400> 20

Met Asp Thr Leu Leu Lys Thr Pro Asn Asn Leu Glu Phe Leu Asn Pro
1 5 10 15

His His Gly Phe Ala Val Lys Ala Ser Thr Phe Arg Ser Glu Lys His
20 25 30

His Asn Phe Gly Ser Arg Lys Phe Cys Glu Thr Leu Gly Arg Ser Val
35 40 45

Cys Val Lys Gly Ser Ser Ser Ala Leu Leu Glu Leu Val Pro Glu Thr
50 55 60

Lys Lys Glu Asn Leu Asp Phe Glu Leu Pro Met Tyr Asp Pro Ser Lys
65 70 75 80

Gly Val Val Val Asp Leu Ala Val Val Gly Gly Gly Pro Ala Gly Leu
85 90 95

Ala	Val	Ala	Gln	Gln	Val	Ser	Glu	Ala	Gly	Leu	Ser	Val	Cys	Ser	Ile	100	105	110
Asp	Pro	Asn	Pro	Lys	Leu	Ile	Trp	Pro	Asn	Asn	Tyr	Gly	Val	Trp	Val	115	120	125
Asp	Glu	Phe	Glu	Ala	Met	Asp	Leu	Leu	Asp	Cys	Leu	Asp	Ala	Thr	Trp	130	135	140
Ser	Gly	Ala	Ala	Val	Tyr	Ile	Asp	Asp	Asn	Thr	Ala	Lys	Asp	Leu	His	145	150	155
Arg	Pro	Tyr	Gly	Arg	Val	Asn	Arg	Lys	Gln	Leu	Lys	Ser	Lys	Met	Met	165	170	175
Gln	Lys	Cys	Ile	Met	Asn	Gly	Val	Lys	Phe	His	Gln	Ala	Lys	Val	Ile	180	185	190
Lys	Val	Ile	His	Glu	Glu	Ser	Lys	Ser	Met	Leu	Ile	Cys	Asn	Asp	Gly	195	200	205
Ile	Thr	Ile	Gln	Ala	Thr	Val	Val	Leu	Asp	Ala	Thr	Gly	Phe	Ser	Arg	210	215	220
Ser	Leu	Val	Gln	Tyr	Asp	Lys	Pro	Tyr	Asn	Pro	Gly	Tyr	Gln	Val	Ala	225	230	235
Tyr	Gly	Ile	Leu	Ala	Glu	Val	Glu	Glu	His	Pro	Phe	Asp	Val	Asn	Lys	245	250	255
Met	Val	Phe	Met	Asp	Trp	Arg	Asp	Ser	His	Leu	Lys	Asn	Asn	Thr	Asp	260	265	270
Leu	Lys	Glu	Arg	Asn	Ser	Arg	Ile	Pro	Thr	Phe	Leu	Tyr	Ala	Met	Pro	275	280	285
Phe	Ser	Ser	Asn	Arg	Ile	Phe	Leu	Glu	Glu	Thr	Ser	Leu	Val	Ala	Arg	290	295	300
Pro	Gly	Leu	Arg	Ile	Asp	Asp	Ile	Gln	Glu	Arg	Met	Val	Ala	Arg	Leu	305	310	315
Asn	His	Leu	Gly	Ile	Lys	Val	Lys	Ser	Ile	Glu	Glu	Asp	Glu	His	Cys	325	330	335

Leu Ile Pro Met Gly Gly Pro Leu Pro Val Leu Pro Gln Arg Val Val
 340 345 350

Gly Ile Gly Gly Thr Ala Gly Met Val His Pro Ser Thr Gly Tyr Met
 355 360 365

Val Ala Arg Thr Leu Ala Ala Ala Pro Val Val Ala Asn Ala Ile Ile
 370 375 380

Gln Tyr Leu Gly Ser Glu Arg Ser His Ser Gly Asn Glu Leu Ser Thr
 385 390 395 400

Ala Val Trp Lys Asp Leu Trp Pro Ile Glu Arg Arg Arg Gln Arg Glu
 405 410 415

Phe Phe Cys Phe Gly Met Asp Ile Leu Leu Lys Leu Asp Leu Pro Ala
 420 425 430

Thr Arg Arg Phe Phe Asp Ala Phe Phe Asp Leu Glu Pro Arg Tyr Trp
 435 440 445

His Gly Phe Leu Ser Ser Arg Leu Phe Leu Pro Glu Leu Ile Val Phe
 450 455 460

Gly Leu Ser Leu Phe Ser His Ala Ser Asn Thr Ser Arg Phe Glu Ile
 465 470 475 480

Met Thr Lys Gly Thr Val Pro Leu Val Asn Met Ile Asn Asn Leu Leu
 485 490 495

Gln Asp Lys Glu
 500

<210> 21

<211> 195

<212> DNA

<213> Potato

<220>

<221> Intron

<400> 21

tacgtaagtt tctgcttcta cctttgatat atatataata attatcatta attagtagta 60

atataatatt tcaaatatatt ttttcaaaat aaaagaatgt agtatatagc aattgctttt 120

ctgtagttaa taagtgtgta tattttaatt tataactttt ctaatatatg accaaaattt 180
gttgatgtgc agctg 195

<210> 22

<211> 1155

<212> DNA

<213> Haematococcus pluvialis

<220>

<221> CDS

<222> (6)..(995)

<400> 22

gaagc atg cag cta gca gcg aca gta atg ttg gag cag ctt acc gga agc 50
Met Gln Leu Ala Ala Thr Val Met Leu Glu Gln Leu Thr Gly Ser
1 5 10 15

gct gag gca ctc aag gag aag gag aag gag gtt gca ggc agc tct gac 98
Ala Glu Ala Leu Lys Glu Lys Glu Lys Glu Val Ala Gly Ser Ser Asp
20 25 30

gtg ttg cgt aca tgg gcg acc cag tac tcg ctt ccg tca gag gag tca 146
Val Leu Arg Thr Trp Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu Ser
35 40 45

gac gcg gcc cgc ccg gga ctg aag aat gcc tac aag cca cca cct tcc 194
Asp Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser
50 55 60

gac aca aag ggc atc aca atg gcg cta gct gtc atc ggc tcc tgg gcc 242
Asp Thr Lys Gly Ile Thr Met Ala Leu Ala Val Ile Gly Ser Trp Ala
65 70 75

gca gtg ttc ctc cac gcc att ttt caa atc aag ctt ccg acc tcc ttg 290
Ala Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu
80 85 90 95

gac cag ctg cac tgg ctg ccc gtg tca gat gcc aca gct cag ctg gtt 338
Asp Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val
100 105 110

agc ggc agc agc agc ctg ctg cac atc gtc gta gta ttc ttt gtc ctg 386
Ser Gly Ser Ser Ser Leu Leu His Ile Val Val Val Phe Phe Val Leu
115 120 125

gag ttc ctg tac aca ggc ctt ttt atc acc acg cat gat gct atg cat 434
Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala Met His
130 135 140

ggc acc atc gcc atg aga aac agg cag ctt aat gac ttc ttg ggc aga 482

Gly Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg	
145 150 155	
gta tgc atc tcc ttg tac gcc tgg ttt gat tac aac atg ctg cac cgc	530
Val Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg	
160 165 170 175	
aag cat tgg gag cac cac aac cac act ggc gag gtg ggc aag gac cct	578
Lys His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys Asp Pro	
180 185 190	
gac ttc cac agg gga aac cct ggc att gtg ccc tgg ttt gcc agc ttc	626
Asp Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala Ser Phe	
195 200 205	
atg tcc agc tac atg tcg atg tgg cag ttt gcg cgc ctc gca tgg tgg	674
Met Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala Trp Trp	
210 215 220	
acg gtg gtc atg cag ctg ctg ggt gcg cca atg gcg aac ctg ctg gtg	722
Thr Val Val Met Gln Leu Leu Gly Ala Pro Met Ala Asn Leu Leu Val	
225 230 235	
ttc atg gcg gcc gcg ccc atc ctg tcc gcc ttc cgc ttg ttc tac ttt	770
Phe Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe	
240 245 250 255	
ggc acg tac atg ccc cac aag cct gag cct ggc gcc gcg tca ggc tct	818
Gly Thr Tyr Met Pro His Lys Pro Glu Pro Gly Ala Ala Ser Gly Ser	
260 265 270	
tca cca gcc gtc atg aac tgg tgg aag tcg cgc act agc cag gcg tcc	866
Ser Pro Ala Val Met Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser	
275 280 285	
gac ctg gtc agc ttt ctg acc tgc tac cac ttc gac ctg cac tgg gag	914
Asp Leu Val Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu	
290 295 300	
cac cac cgc tgg ccc ttt gcc ccc tgg tgg gag ctg ccc aac tgc cgc	962
His His Arg Trp Pro Phe Ala Pro Trp Trp Glu Leu Pro Asn Cys Arg	
305 310 315	
cgc ctg tct ggc cga ggt ctg gtt cct gcc tag ctggacacac tgcagtgggc	1015
Arg Leu Ser Gly Arg Gly Leu Val Pro Ala	
320 325	
cctgctgccca gctgggcatg caggttgtgg caggactggg tgagggtgaaa agctgcaggc	1075
gctgctgccg gacacgctgc atgggctacc ctgtgtagct gccgccacta ggggaggggg	1135
ttttagctg tcgagcttgc	1155
<210> 23	
<211> 329	
<212> PRT	

<213> Haematococcus pluvialis

<400> 23

Met Gln Leu Ala Ala Thr Val Met Leu Glu Gln Leu Thr Gly Ser Ala
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Glu Ala Leu Lys Glu Lys Glu Lys Glu Val Ala Gly Ser Ser Asp Val
20 25 30

Leu Arg Thr Trp Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu Ser Asp
35 40 45

Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser Asp
50 55 60

Thr Lys Gly Ile Thr Met Ala Leu Ala Val Ile Gly Ser Trp Ala Ala
65 70 75 80

Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu Asp
85 90 95

Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val Ser
100 105 110

Gly Ser Ser Ser Leu Leu His Ile Val Val Val Phe Phe Val Leu Glu
115 120 125

Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala Met His Gly
130 135 140

Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg Val
145 150 155 160

Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg Lys
165 170 175

His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys Asp Pro Asp
180 185 190

Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala Ser Phe Met
195 200 205

Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala Trp Trp Thr
210 215 220

Val Val Met Gln Leu Leu Gly Ala Pro Met Ala Asn Leu Leu Val Phe
225 230 235 240

Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe Gly
245 250 255

Thr Tyr Met Pro His Lys Pro Glu Pro Gly Ala Ala Ser Gly Ser Ser
260 265 270

Pro Ala Val Met Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser Asp
275 280 285

Leu Val Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu His
290 295 300

His Arg Trp Pro Phe Ala Pro Trp Trp Glu Leu Pro Asn Cys Arg Arg
305 310 315 320

Leu Ser Gly Arg Gly Leu Val Pro Ala
325

<210> 24

<211> 1111

<212> DNA

<213> Haematococcus pluvialis

<220>

<221> CDS

<222> (4)..(951)

<400> 24

tgc atg cta gag gca ctc aag gag aag gag aag gag gtt gca ggc agc 48
Met Leu Glu Ala Leu Lys Glu Lys Glu Lys Glu Val Ala Gly Ser

1

5

10

15

tct gac gtg ttg cgt aca tgg gcg acc cag tac tcg ctt ccg tca gaa 96
Ser Asp Val Leu Arg Thr Trp Ala Thr Gln Tyr Ser Leu Pro Ser Glu
20 25 30

gag tca gac gcg gcc cgc ccg gga ctg aag aat gcc tac aag cca cca 144
Glu Ser Asp Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro
35 40 45

cct tcc gac aca aag ggc atc aca atg gcg cta gct gtc atc ggc tcc 192
Pro Ser Asp Thr Lys Gly Ile Thr Met Ala Leu Ala Val Ile Gly Ser
50 55 60

tgg gcc gca gtg ttc ctc cac gcc att ttt caa atc aag ctt ccg acc	240
Trp Ala Ala Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr	
65 70 75	
tcc ttg gac cag ctg cac tgg ctg ccc gtg tca gat gcc aca gct cag	288
Ser Leu Asp Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln	
80 85 90 95	
ctg gtt agc ggc agc agc agc ctg ctg cac atc gtc gta gta ttc ttt	336
Leu Val Ser Gly Ser Ser Ser Leu Leu His Ile Val Val Val Phe Phe	
100 105 110	
gtc ctg gag ttc ctg tac aca ggc ctt ttt atc acc acg cat gat gct	384
Val Leu Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala	
115 120 125	
atg cat ggc acc atc gcc atg aga aac agg cag ctt aat gac ttc ttg	432
Met His Gly Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu	
130 135 140	
ggc aga gta tgc atc tcc ttg tac gcc tgg ttt gat tac aac atg ctg	480
Gly Arg Val Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu	
145 150 155	
cac cgc aag cat tgg gag cac cac aac cac act ggc gag gtg ggc aag	528
His Arg Lys His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys	
160 165 170 175	
gac cct gac ttc cac agg gga aac cct ggc att gtg ccc tgg ttt gcc	576
Asp Pro Asp Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala	
180 185 190	
agc ttc atg tcc agc tac atg tcg atg tgg cag ttt gcg cgc ctc gca	624
Ser Phe Met Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala	
195 200 205	
tgg tgg acg gtg gtc atg cag ctg ctg ggt gcg cca atg gcg aac ctg	672
Trp Trp Thr Val Val Met Gln Leu Leu Gly Ala Pro Met Ala Asn Leu	
210 215 220	
ctg gtg ttc atg gcg gcc gcg ccc atc ctg tcc gcc ttc cgc ttg ttc	720
Leu Val Phe Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe	
225 230 235	
tac ttt ggc acg tac atg ccc cac aag cct gag cct ggc gcc gcg tca	768
Tyr Phe Gly Thr Tyr Met Pro His Lys Pro Glu Pro Gly Ala Ala Ser	
240 245 250 255	
ggc tct tca cca gcc gtc atg aac tgg tgg aag tcg cgc act agc cag	816
Gly Ser Ser Pro Ala Val Met Asn Trp Trp Lys Ser Arg Thr Ser Gln	
260 265 270	
gcg tcc gac ctg gtc agc ttt ctg acc tgc tac cac ttc gac ctg cac	864
Ala Ser Asp Leu Val Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His	
275 280 285	
tgg gag cac cac cgc tgg ccc ttc gcc ccc tgg tgg gag ctg ccc aac	912
Trp Glu His His Arg Trp Pro Phe Ala Pro Trp Trp Glu Leu Pro Asn	

290	295	300	
tgc cgc cgc ctg tct ggc cga ggt ctg gtt cct gcc tag ctggacacac			961
Cys Arg Arg Leu Ser Gly Arg Gly Leu Val Pro Ala			
305	310	315	
tcgagtgggc cctgctgcca gctgggcatg caggttgtgg caggactggg tgagggtgaaa			1021
agctgcaggc gctgctgccg gacacgttgc atgggctacc ctgtgtagct gccgccacta			1081
ggggagggggg tttgtagctg tcgagcttgc			1111
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<213>	Haematococcus pluvialis		
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Asp Val Leu Arg Thr Trp Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu			
	20	25	30
Ser Asp Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro			
	35	40	45
Ser Asp Thr Lys Gly Ile Thr Met Ala Leu Ala Val Ile Gly Ser Trp			
	50	55	60
Ala Ala Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser			
65	70	75	80
Leu Asp Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln Leu			
	85	90	95
Val Ser Gly Ser Ser Ser Leu Leu His Ile Val Val Val Phe Phe Val			
	100	105	110
Leu Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala Met			
	115	120	125
His Gly Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly			
	130	135	140
Arg Val Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu His			

145		150		155		160
Arg Lys His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys Asp						
	165			170		175
Pro Asp Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala Ser						
	180		185			190
Phe Met Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala Trp						
	195		200			205
Trp Thr Val Val Met Gln Leu Leu Gly Ala Pro Met Ala Asn Leu Leu						
	210		215		220	
Val Phe Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr						
225		230		235		240
Phe Gly Thr Tyr Met Pro His Lys Pro Glu Pro Gly Ala Ala Ser Gly						
	245		250			255
Ser Ser Pro Ala Val Met Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala						
	260		265			270
Ser Asp Leu Val Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp						
	275		280		285	
Glu His His Arg Trp Pro Phe Ala Pro Trp Trp Glu Leu Pro Asn Cys						
	290		295		300	
Arg Arg Leu Ser Gly Arg Gly Leu Val Pro Ala						
305		310		315		

<210> 26

<211> 1031

<212> DNA

<213> Haematococcus pluvialis

<220>

<221> CDS

<222> (6)..(1031)

<400> 26

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Met Gln Leu Ala Thr Val Met Leu Glu Gln Leu Thr Gly Ser																
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gct	gag	gca	ctc	aag	gag	aag	gag	aag	gag	gtt	gca	ggc	agc	tct	gac	98
Ala	Glu	Ala	Leu	Lys	Glu	Lys	Glu	Lys	Glu	Val	Ala	Gly	Ser	Ser	Asp	
			20					25					30			
gtg	ttg	cgt	aca	tgg	gcg	acc	cag	tac	tcg	ctt	ccg	tca	gag	gag	tca	146
Val	Leu	Arg	Thr	Trp	Ala	Thr	Gln	Tyr	Ser	Leu	Pro	Ser	Glu	Glu	Ser	
			35				40						45			
gac	gcg	gcc	cgc	ccg	gga	ctg	aag	aat	gcc	tac	aag	cca	cca	cct	tcc	194
Asp	Ala	Ala	Arg	Pro	Gly	Leu	Lys	Asn	Ala	Tyr	Lys	Pro	Pro	Pro	Ser	
		50					55					60				
gac	aca	aag	ggc	atc	aca	atg	gcg	cta	gct	gtc	atc	ggc	tcc	tgg	gct	242
Asp	Thr	Lys	Gly	Ile	Thr	Met	Ala	Leu	Ala	Val	Ile	Gly	Ser	Trp	Ala	
	65					70					75					
gca	gtg	ttc	ctc	cac	gcc	att	ttt	caa	atc	aag	ctt	ccg	acc	tcc	ttg	290
Ala	Val	Phe	Leu	His	Ala	Ile	Phe	Gln	Ile	Lys	Leu	Pro	Thr	Ser	Leu	
80				85				90							95	
gac	cag	ctg	cac	tgg	ctg	ccc	gtg	tca	gat	gcc	aca	gct	cag	ctg	gtt	338
Asp	Gln	Leu	His	Trp	Leu	Pro	Val	Ser	Asp	Ala	Thr	Ala	Gln	Leu	Val	
			100					105					110			
agc	ggc	agc	agc	agc	ctg	ctg	cac	atc	gtc	gta	gta	ttc	ttt	gtc	ctg	386
Ser	Gly	Ser	Ser	Ser	Leu	Leu	His	Ile	Val	Val	Val	Phe	Phe	Val	Leu	
		115					120					125				
gag	ttc	ctg	tac	aca	ggc	ctt	ttt	atc	acc	acg	cat	gat	gct	atg	cat	434
Glu	Phe	Leu	Tyr	Thr	Gly	Leu	Phe	Ile	Thr	Thr	His	Asp	Ala	Met	His	
		130				135						140				
ggc	acc	atc	gcc	atg	aga	aac	agg	cag	ctt	aat	gac	ttc	ttg	ggc	aga	482
Gly	Thr	Ile	Ala	Met	Arg	Asn	Arg	Gln	Leu	Asn	Asp	Phe	Leu	Gly	Arg	
	145					150				155						
gta	tgc	atc	tcc	ttg	tac	gcc	tgg	ttt	gat	tac	aac	atg	ctg	cac	cgc	530
Val	Cys	Ile	Ser	Leu	Tyr	Ala	Trp	Phe	Asp	Tyr	Asn	Met	Leu	His	Arg	
160				165				170					175			
aag	cat	tgg	gag	cac	cac	aac	cac	act	ggc	gag	gtg	ggc	aag	gac	cct	578
Lys	His	Trp	Glu	His	His	Asn	His	Thr	Gly	Glu	Val	Gly	Lys	Asp	Pro	
			180					185					190			
gac	ttc	cac	agg	gga	aac	cct	ggc	att	gtg	ccc	tgg	ttt	gcc	agc	ttc	626
Asp	Phe	His	Arg	Gly	Asn	Pro	Gly	Ile	Val	Pro	Trp	Phe	Ala	Ser	Phe	
		195				200						205				
atg	tcc	agc	tac	atg	tcg	atg	tgg	cag	ttt	gcg	cgc	ctc	gca	tgg	tgg	674
Met	Ser	Ser	Tyr	Met	Ser	Met	Trp	Gln	Phe	Ala	Arg	Leu	Ala	Trp	Trp	
		210				215						220				
acg	gtg	gtc	atg	cag	ctg	ctg	ggt	gcg	cca	atg	gcg	aac	ctg	ctg	gtg	722
Thr	Val	Val	Met	Gln	Leu	Leu	Gly	Ala	Pro	Met	Ala	Asn	Leu	Leu	Val	
	225				230			235								
ttc	atg	gcg	gcc	gcg	ccc	atc	ctg	tcc	gcc	ttc	cgc	ttg	ttc	tac	ttt	770

Phe Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe
 240 245 250 255
 ggc acg tac atg ccc cac aag cct gag cct ggc gcc gcg tca ggc tct 818
 Gly Thr Tyr Met Pro His Lys Pro Glu Pro Gly Ala Ala Ser Gly Ser
 260 265 270
 tca cca gcc gtc atg aac tgg tgg aag tcg cgc act agc cag gcg tcc 866
 Ser Pro Ala Val Met Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser
 275 280 285
 gac ctg gtc agc ttt ctg acc tgc tac cac ttc gac ctg cac tgg gag 914
 Asp Leu Val Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu
 290 295 300
 cac cac cgc tgg ccc ttt gcc ccc tgg tgg gag ctg ccc aac tgc cgc 962
 His His Arg Trp Pro Phe Ala Pro Trp Trp Glu Leu Pro Asn Cys Arg
 305 310 315
 cgc ctg tct ggc cga ggt ctg gtt cct gcc gag caa aaa ctc atc tca 1010
 Arg Leu Ser Gly Arg Gly Leu Val Pro Ala Glu Gln Lys Leu Ile Ser
 320 325 330 335
 gaa gag gat ctg aat agc tag 1031
 Glu Glu Asp Leu Asn Ser
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<210> 27

<211> 341

<212> PRT

<213> Haematococcus pluvialis

<400> 27

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Glu Ala Leu Lys Glu Lys Glu Lys Glu Val Ala Gly Ser Ser Asp Val
 20 25 30

Leu Arg Thr Trp Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu Ser Asp
 35 40 45

Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser Asp
 50 55 60

Thr Lys Gly Ile Thr Met Ala Leu Ala Val Ile Gly Ser Trp Ala Ala
 65 70 75 80

Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu Asp
 85 90 95

Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val Ser
 100 105 110

Gly Ser Ser Ser Leu Leu His Ile Val Val Val Phe Phe Val Leu Glu
 115 120 125

Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala Met His Gly
 130 135 140

Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg Val
 145 150 155 160

Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg Lys
 165 170 175

His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys Asp Pro Asp
 180 185 190

Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala Ser Phe Met
 195 200 205

Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala Trp Trp Thr
 210 215 220

Val Val Met Gln Leu Leu Gly Ala Pro Met Ala Asn Leu Leu Val Phe
 225 230 235 240

Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe Gly
 245 250 255

Thr Tyr Met Pro His Lys Pro Glu Pro Gly Ala Ala Ser Gly Ser Ser
 260 265 270

Pro Ala Val Met Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser Asp
 275 280 285

Leu Val Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu His
 290 295 300

His Arg Trp Pro Phe Ala Pro Trp Trp Glu Leu Pro Asn Cys Arg Arg
 305 310 315 320

Leu Ser Gly Arg Gly Leu Val Pro Ala Glu Gln Lys Leu Ile Ser Glu

325

330

335

Glu Asp Leu Asn Ser
340

<210> 28

<211> 777

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> promoter

<400> 28

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tagtttcaaaa acaacagtaa ctgtggccaa cttagttttg aaacaacact aactgggtcga	120
agcaaaaaga aaaaagagtt tcatcatata tctgatttga tggactgttt ggagttagga	180
ccaaacatta tctacaaaca aagacttttc tcctaacttg tgattccttc ttaaaccccta	240
ggggtaatat tctattttcc aaggatcttt agttaaaggc aaatccggga aattattgta	300
atcatttggg gaaacatata aaagatttga gttagatgga agtgacgatt aatccaaaca	360
tatatatctc tttctttctta tttcccaaata taacagacaa aagtagaata ttggctttta	420
acaccaatat aaaaacttgc ttcacaccta aaacttttg tttacttttag ggtaagtgca	480
aaaagccaac caaatccacc tgcactgatt tgacgtttac aaacgccgtt aagtcgatgt	540
ccgttgattt aaacagtgtc ttgtaattaa aaaaatcagt ttacataaat ggaaaattta	600
tcacttagtt ttcatcaact tctgaactta cctttcatgg attaggcaat actttccatt	660
tttagtaact caagtggacc ctttacttct tcaactccat ctctctcttt ctatttccact	720
tctttcttct cattatatct cttgtcctct ccaccaaata tcttcaacaa aaagctt	777

<210> 29

<211> 22

<212> DNA

<213> Unknown

<220>

<221> Primer_bind

<223> Artificial sequence

<400> 29
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<210> 30

<211> 24

<212> DNA

<213> Unknown

<220>

<221> Primer_bind

<223> Artificial sequence

<400> 30
gaagcatgca gctagcagcg acag 24

<210> 31

<211> 30

<212> DNA

<213> Unknown

<220>

<221> Primer_bind

<223> Artificial sequence

<400> 31
tgcattgctag aggcactcaa ggagaaggag 30

<210> 32

<211> 59

<212> DNA

<213> Unknown

<220>

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<223> Artificial sequence

<400> 32
ctagctattc agatcctctt ctgagatgag tttttgctcg gcaggaacca gacctcggc 59

<210> 33

<211> 28

<212> DNA

<213> Unknown

<220>

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<223> Artificial sequence

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gagctcactc actgatttcc attgcttg

28

<210> 34

<211> 37

<212> DNA

<213> Unknown

<220>

<221> Primer_bind

<223> Artificial sequence

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cgccgttaag tcgatgtccg ttgatttaaa cagtgtc

37

<210> 35

<211> 34

<212> DNA

<213> Unknown

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<221> Primer_bind

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<210> 36

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<212> DNA

<213> Unknown

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<221> Primer_bind

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<211> 212

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<221> Intron

<223> Artificial sequence

<400> 37

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gtagtaatat aatatttcaa atattttttt caaaataaaa gaatgtagta tatagcaatt 120

gcttttctgt agtttataag tgtgtatatt ttaatttata acttttctaa tatatgacca 180

aaatttggtg atgtgcagg atcaccggat cc 212

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<212> DNA

<213> Tagetes erecta

<220>

<221> CDS

<222> (141)..(1691)

<400> 38

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gatacaaggc gtgactggat atttctctct cgttcctaac aacagcaacg aagaagaaaa 120

agaatcatta ctaacaatca atg agt atg aga gct gga cac atg acg gca aca 173

Met Ser Met Arg Ala Gly His Met Thr Ala Thr
1 5 10

atg gcg gct ttt aca tgc cct agg ttt atg act agc atc aga tac acg 221

Met	Ala	Ala	Phe	Thr	Cys	Pro	Arg	Phe	Met	Thr	Ser	Ile	Arg	Tyr	Thr	
			15					20					25			
aag	caa	att	aag	tgc	aac	gct	gct	aaa	agc	cag	cta	gtc	ggt	aaa	caa	269
Lys	Gln	Ile	Lys	Cys	Asn	Ala	Ala	Lys	Ser	Gln	Leu	Val	Val	Lys	Gln	
		30					35					40				
gag	att	gag	gag	gaa	gaa	gat	tat	gtg	aaa	gcc	ggt	gga	tcg	gag	ctg	317
Glu	Ile	Glu	Glu	Glu	Glu	Asp	Tyr	Val	Lys	Ala	Gly	Gly	Ser	Glu	Leu	
	45					50					55					
ctt	ttt	ggt	caa	atg	caa	cag	aat	aag	tcc	atg	gat	gca	cag	tct	agc	365
Leu	Phe	Val	Gln	Met	Gln	Gln	Asn	Lys	Ser	Met	Asp	Ala	Gln	Ser	Ser	
60					65				70						75	
cta	tcc	caa	aag	ctc	cca	agg	gta	cca	ata	gga	gga	gga	gga	gac	agt	413
Leu	Ser	Gln	Lys	Leu	Pro	Arg	Val	Pro	Ile	Gly	Gly	Gly	Gly	Asp	Ser	
				80				85						90		
aac	tgt	ata	ctg	gat	ttg	ggt	gta	att	ggt	tgt	ggt	cct	gct	ggc	ctt	461
Asn	Cys	Ile	Leu	Asp	Leu	Val	Val	Ile	Gly	Cys	Gly	Pro	Ala	Gly	Leu	
		95					100					105				
gct	ctt	gct	gga	gaa	tca	gcc	aag	cta	ggc	ttg	aat	gtc	gca	ctt	atc	509
Ala	Leu	Ala	Gly	Glu	Ser	Ala	Lys	Leu	Gly	Leu	Asn	Val	Ala	Leu	Ile	
	110						115					120				
ggc	cct	gat	ctt	cct	ttt	aca	aat	aac	tat	ggt	ggt	tgg	gag	gat	gaa	557
Gly	Pro	Asp	Leu	Pro	Phe	Thr	Asn	Asn	Tyr	Gly	Val	Trp	Glu	Asp	Glu	
	125					130					135					
ttt	ata	ggt	ctt	gga	ctt	gag	ggc	tgt	att	gaa	cat	ggt	tgg	cga	gat	605
Phe	Ile	Gly	Leu	Gly	Leu	Glu	Gly	Cys	Ile	Glu	His	Val	Trp	Arg	Asp	
140					145				150						155	
act	gta	gta	tat	ctt	gat	gac	aac	gat	ccc	att	ctc	ata	ggt	cgt	gcc	653
Thr	Val	Val	Tyr	Leu	Asp	Asp	Asn	Asp	Pro	Ile	Leu	Ile	Gly	Arg	Ala	
				160					165					170		
tat	gga	cga	ggt	agt	cgt	gat	tta	ctt	cac	gag	gag	ttg	ttg	act	agg	701
Tyr	Gly	Arg	Val	Ser	Arg	Asp	Leu	Leu	His	Glu	Glu	Leu	Leu	Thr	Arg	
			175					180					185			
tgc	atg	gag	tca	ggc	ggt	tca	tat	ctg	agc	tcc	aaa	gtg	gaa	cgg	att	749
Cys	Met	Glu	Ser	Gly	Val	Ser	Tyr	Leu	Ser	Ser	Lys	Val	Glu	Arg	Ile	
	190						195					200				
act	gaa	gct	cca	aat	ggc	cta	agt	ctc	ata	gag	tgt	gaa	ggc	aat	atc	797
Thr	Glu	Ala	Pro	Asn	Gly	Leu	Ser	Leu	Ile	Glu	Cys	Glu	Gly	Asn	Ile	
	205					210					215					
aca	att	cca	tgc	agg	ctt	gct	act	gtc	gct	tct	gga	gca	gct	tct	gga	845
Thr	Ile	Pro	Cys	Arg	Leu	Ala	Thr	Val	Ala	Ser	Gly	Ala	Ala	Ser	Gly	
220					225				230						235	
aaa	ctt	ttg	cag	tat	gaa	ctt	ggc	ggt	ccc	cgt	ggt	tgc	ggt	caa	aca	893
Lys	Leu	Leu	Gln	Tyr	Glu	Leu	Gly	Gly	Pro	Arg	Val	Cys	Val	Gln	Thr	
			240						245					250		
gct	tat	ggt	ata	gag	ggt	gag	ggt	gaa	agc	ata	ccc	tat	gat	cca	agc	941

Ala Tyr Gly Ile Glu Val Glu Val Glu Ser Ile Pro Tyr Asp Pro Ser	
255 260 265	
cta atg gtt ttc atg gat tat aga gac tac acc aaa cat aaa tct caa	989
Leu Met Val Phe Met Asp Tyr Arg Asp Tyr Thr Lys His Lys Ser Gln	
270 275 280	
tca cta gaa gca caa tat cca aca ttt ttg tat gtc atg cca atg tct	1037
Ser Leu Glu Ala Gln Tyr Pro Thr Phe Leu Tyr Val Met Pro Met Ser	
285 290 295	
cca act aaa gta ttc ttt gag gaa act tgt ttg gct tca aaa gag gcc	1085
Pro Thr Lys Val Phe Phe Glu Glu Thr Cys Leu Ala Ser Lys Glu Ala	
300 305 310 315	
atg cct ttt gag tta ttg aag aca aaa ctc atg tca aga tta aag act	1133
Met Pro Phe Glu Leu Leu Lys Thr Lys Leu Met Ser Arg Leu Lys Thr	
320 325 330	
atg ggg atc cga ata acc aaa act tat gaa gag gaa tgg tca tat att	1181
Met Gly Ile Arg Ile Thr Lys Thr Tyr Glu Glu Glu Trp Ser Tyr Ile	
335 340 345	
cca gta ggt gga tcc tta cca aat acc gag caa aag aac ctt gca ttt	1229
Pro Val Gly Gly Ser Leu Pro Asn Thr Glu Gln Lys Asn Leu Ala Phe	
350 355 360	
ggg gct gct gct agc atg gtg cat cca gcc aca gga tat tcg gtt gta	1277
Gly Ala Ala Ala Ser Met Val His Pro Ala Thr Gly Tyr Ser Val Val	
365 370 375	
aga tca ctg tca gaa gct cct aat tat gca gca gta att gca aag att	1325
Arg Ser Leu Ser Glu Ala Pro Asn Tyr Ala Ala Val Ile Ala Lys Ile	
380 385 390 395	
tta ggg aaa gga aat tca aaa cag atg ctt gat cat gga aga tac aca	1373
Leu Gly Lys Gly Asn Ser Lys Gln Met Leu Asp His Gly Arg Tyr Thr	
400 405 410	
acc aac atc tca aag caa gct tgg gaa aca ctt tgg ccc ctt gaa agg	1421
Thr Asn Ile Ser Lys Gln Ala Trp Glu Thr Leu Trp Pro Leu Glu Arg	
415 420 425	
aaa aga cag aga gca ttc ttt ctc ttt gga tta gca ctg att gtc cag	1469
Lys Arg Gln Arg Ala Phe Phe Leu Phe Gly Leu Ala Leu Ile Val Gln	
430 435 440	
atg gat att gag ggg acc cgc aca ttc ttc cgg act ttc ttc cgc ttg	1517
Met Asp Ile Glu Gly Thr Arg Thr Phe Phe Arg Thr Phe Phe Arg Leu	
445 450 455	
ccc aca tgg atg tgg tgg ggg ttt ctt gga tct tcg tta tca tca act	1565
Pro Thr Trp Met Trp Trp Gly Phe Leu Gly Ser Ser Leu Ser Ser Thr	
460 465 470 475	
gac ttg ata ata ttt gcg ttt tac atg ttt atc ata gca ccg cat agc	1613
Asp Leu Ile Ile Phe Ala Phe Tyr Met Phe Ile Ile Ala Pro His Ser	
480 485 490	
ctg aga atg ggt ctg gtt aga cat ttg ctt tct gac ccg aca gga gga	1661

Leu Arg Met Gly Leu Val Arg His Leu Leu Ser Asp Pro Thr Gly Gly
 495 500 505

aca atg tta aaa gcg tat ctc acg ata taa ataactctag tcgcgatcag 1711
 Thr Met Leu Lys Ala Tyr Leu Thr Ile
 510 515

tttagattat aggcacatct tgcatatata tatgtataaaa ccttatgtgt gctgtatcct 1771
 tacatcaaca cagtcattaa ttgtatttct tggggtaatg ctgatgaagt attttctgg 1830

<210> 39
 <211> 516
 <212> PRT
 <213> Tagetes erecta
 <400> 39

Met Ser Met Arg Ala Gly His Met Thr Ala Thr Met Ala Ala Phe Thr
 1 5 10 15

Cys Pro Arg Phe Met Thr Ser Ile Arg Tyr Thr Lys Gln Ile Lys Cys
 20 25 30

Asn Ala Ala Lys Ser Gln Leu Val Val Lys Gln Glu Ile Glu Glu Glu
 35 40 45

Glu Asp Tyr Val Lys Ala Gly Gly Ser Glu Leu Leu Phe Val Gln Met
 50 55 60

Gln Gln Asn Lys Ser Met Asp Ala Gln Ser Ser Leu Ser Gln Lys Leu
 65 70 75 80

Pro Arg Val Pro Ile Gly Gly Gly Gly Asp Ser Asn Cys Ile Leu Asp
 85 90 95

Leu Val Val Ile Gly Cys Gly Pro Ala Gly Leu Ala Leu Ala Gly Glu
 100 105 110

Ser Ala Lys Leu Gly Leu Asn Val Ala Leu Ile Gly Pro Asp Leu Pro
 115 120 125

Phe Thr Asn Asn Tyr Gly Val Trp Glu Asp Glu Phe Ile Gly Leu Gly
 130 135 140

Leu Glu Gly Cys Ile Glu His Val Trp Arg Asp Thr Val Val Tyr Leu
 145 150 155 160

Asp Asp Asn Asp Pro Ile Leu Ile Gly Arg Ala Tyr Gly Arg Val Ser
 165 170 175

Arg Asp Leu Leu His Glu Glu Leu Leu Thr Arg Cys Met Glu Ser Gly
 180 185 190

Val Ser Tyr Leu Ser Ser Lys Val Glu Arg Ile Thr Glu Ala Pro Asn
 195 200 205

Gly Leu Ser Leu Ile Glu Cys Glu Gly Asn Ile Thr Ile Pro Cys Arg
 210 215 220

Leu Ala Thr Val Ala Ser Gly Ala Ala Ser Gly Lys Leu Leu Gln Tyr
 225 230 235 240

Glu Leu Gly Gly Pro Arg Val Cys Val Gln Thr Ala Tyr Gly Ile Glu
 245 250 255

Val Glu Val Glu Ser Ile Pro Tyr Asp Pro Ser Leu Met Val Phe Met
 260 265 270

Asp Tyr Arg Asp Tyr Thr Lys His Lys Ser Gln Ser Leu Glu Ala Gln
 275 280 285

Tyr Pro Thr Phe Leu Tyr Val Met Pro Met Ser Pro Thr Lys Val Phe
 290 295 300

Phe Glu Glu Thr Cys Leu Ala Ser Lys Glu Ala Met Pro Phe Glu Leu
 305 310 315 320

Leu Lys Thr Lys Leu Met Ser Arg Leu Lys Thr Met Gly Ile Arg Ile
 325 330 335

Thr Lys Thr Tyr Glu Glu Glu Trp Ser Tyr Ile Pro Val Gly Gly Ser
 340 345 350

Leu Pro Asn Thr Glu Gln Lys Asn Leu Ala Phe Gly Ala Ala Ala Ser
 355 360 365

Met Val His Pro Ala Thr Gly Tyr Ser Val Val Arg Ser Leu Ser Glu
 370 375 380

Ala Pro Asn Tyr Ala Ala Val Ile Ala Lys Ile Leu Gly Lys Gly Asn
 385 390 395 400

Ser Lys Gln Met Leu Asp His Gly Arg Tyr Thr Thr Asn Ile Ser Lys
 405 410 415

Gln Ala Trp Glu Thr Leu Trp Pro Leu Glu Arg Lys Arg Gln Arg Ala
 420 425 430

Phe Phe Leu Phe Gly Leu Ala Leu Ile Val Gln Met Asp Ile Glu Gly
 435 440 445

Thr Arg Thr Phe Phe Arg Thr Phe Phe Arg Leu Pro Thr Trp Met Trp
 450 455 460

Trp Gly Phe Leu Gly Ser Ser Leu Ser Ser Thr Asp Leu Ile Ile Phe
 465 470 475 480

Ala Phe Tyr Met Phe Ile Ile Ala Pro His Ser Leu Arg Met Gly Leu
 485 490 495

Val Arg His Leu Leu Ser Asp Pro Thr Gly Gly Thr Met Leu Lys Ala
 500 505 510

Tyr Leu Thr Ile
 515

<210> 40

<211> 445

<212> DNA

<213> Tagetes erecta

<220>

<221> misc_feature

<222> (1)..(445)

<223> Sense fragment

<400> 40

aagcttgcac gaggcaaagc aaaggttggt tgttggtggt gttgagagac actccaatcc	60
aaacagatac aaggcgtgac tggatatttc tctctcgttc ctaacaacag caacgaagaa	120
gaaaaagaat cattactaac aatcaatgag tatgagagct ggacacatga cggcaacaat	180
ggcggctttt acatgcccta ggtttatgac tagcatcaga tacacgaagc aaattaagtg	240
caacgctgct aaaagccagc tagtcgttaa acaagagatt gaggaggaag aagattatgt	300

gaaagccggt ggatcggagc tgctttttgt tcaaatacaa cagaataagt ccatggatgc 360
 acagtctagc ctatcccaaa agctcccaag ggtaccaata ggaggaggag gagacagtaa 420
 ctgtatactg gatttggttg tcgac 445

<210> 41

<211> 446

<212> DNA

<213> Tagetes erecta

<220>

<221> misc_feature

<222> (1)..(446)

<223> Antisense fragment

<400> 41

gaattcgcac gaggcaaagc aaagggtggt tgttggtggt gttgagagac actccaatcc 60
 aaacagatac aaggcgtgac tggatatttc tctctcgttc ctaacaacag caacgaagaa 120
 gaaaaagaat cattactaac aatcaatgag tatgagagct ggacacatga cggcaacaat 180
 ggcggctttt acatgcccta ggtttatgac tagcatcaga tacacgaagc aaattaagtg 240
 caacgctgct aaaagccagc tagtcggtta acaagagatt gaggaggaag aagattatgt 300
 gaaagccggt ggatcggagc tgctttttgt tcaaatacaa cagaataagt ccatggatgc 360
 acagtctagc ctatcccaaa agctcccaag ggtaccaata ggaggaggag gagacagtaa 420
 ctgtatactg gatttggttg gatcct 446

<210> 42

<211> 393

<212> DNA

<213> Tagetes erecta

<220>

<221> misc_feature

<222> (1)..(393)

<223> Sense fragment

<400> 42

aagcttttga ttagcaactga ttgtccagat ggatattgag gggacccgca cattcttccg 60

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gactttcttc cgcttgccca catggatgtg gtggggggtt cttggatctt cgttatcatc 120
aactgacttg ataatatattg cgttttacat gtttatcata gcaccgcata gcctgagaat 180
gggtctgggt agacatttgc tttctgaccc gacaggagga acaatgttaa aagcgtatct 240
cacgatataa ataactctag tcgcgatcag tttagattat aggcacatct tgcatatata 300
tatgtataaa ccttatgtgt gctgtatcct tacatcaaca cagtcattaa ttgtatttct 360
tggggtaatg ctgatgaagt attttctgtc gac 393

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<210> 43

<211> 397

<212> DNA

<213> Tagetes erecta

<220>

<221> misc_feature

<222> (1)..(397)

<223> Antisense fragment

<400> 43

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gaattctctt tggattagca ctgattgtcc agatggatat tgaggggacc cgcacattct 60
tccggacttt cttccgcttg cccacatgga tgtggtgggg gtttcttgga tcttcgttat 120
catcaactga cttgataata tttgcgtttt acatgtttat catagcaccg catagcctga 180
gaatgggtct ggtagacat ttgctttctg acccgacagg aggaacaatg ttaaaagcgt 240
atctcacgat ataaataact ctagtcgcga tcagtttaga ttataggcac atcttgcata 300
tatatatgta taaaccttat gtgtgctgta tccttacatc aacacagtca ttaattgtat 360
ttcttggggg aatgctgatg aagtattttc tggatcc 397

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<210> 44

<211> 1537

<212> DNA

<213> Unknown

<220>

<221> promoter

<222> (1)..(1537)

<223> Promoter sequence

<400> 44

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gagctctaca aattaggggtt actttattca ttttcatcca ttctctttat tgttaaattt   60
tgtacattta ttcaataata ttatatgttt attacaaatt ctcactttct tattcatacc   120
tattcactca agcctttacc atcttccttt tctattttcaa tactatttct acttcatttt   180
tcacgttttt aacatctttc tttatttctt gtccacttcg tttagggatg cctaagtgtc   240
caaatttcat ctctcgtagt aacacaaaac caatgtaatg ctacttctct ctacattttt   300
aatacaaata aagtgaaca aaatatctat aaataaaca atatatatat tttgttagac   360
gctgtctcaa cccatcaatt aaaaaatttt gttatatttc tactttacct actaaatttg   420
tttctcatat ttacctttta acccccacaa aaaaaaatta taaaaaagaa agaaaaaagc   480
taaaccctat ttaaataagt aactataaga tcttaaaatt atcctcatca gtgtatagtt   540
taattgggta ttaacttata acattatata tctatgacat atactctctc ctagctattt   600
ctcacatttt ttaacttaag aaaatagtc taacatagtc taaaattcaa acatccacat   660
gctctaattt gattaacaaa aagttagaaa tattttattta aataaaaaaag actaataaat   720
atataaaatg aatgttcata cgcagacca tttagagatg agtatgcttt cacatgctga   780
gattattttc aaaactaagg ttgtagcaat attaaatcaa taaaattatt ataaataaca   840
aaattaacct gctcgtgttt gctgtatatg ggaggctaca aaataaatta aactaaagat   900
gattatgttt tagacatttt ttctatctgt attagtttat acatattaat tcaggagctg   960
cacaacccaa ttctattttc gttccttggt ggctgggttt ctcaagaagt tcaatagtca 1020
atattagggt ttattggact tttaatagta tcaacaaat ctatgtgtga acttaaaaat 1080
tgtattaaat atttagggta acctgttgcc gtttttagaa taatgtttct tcttaataca 1140
cgaaagcgta ttgtgtattc attcatttgg cgcctcacat gcttcggttg gctcgcttta 1200
gtctctgcct tctttgtata ttgtactccc cctcttccta tgccacgtgt tctgagctta 1260
acaagccacg ttgcgtgcca ttgccaaaca agtcatttta acttcacaag gtccgatttg 1320
acctccaaaa caacgacaag tttccgaaca gtcgcgaaga tcaagggtat aatcgtcttt 1380
ttgaattcta tttctcttta tttaatagtc cctctcgtgt gatagttttt aaaagatttt 1440
taaaacgtag ctgctgttta agtaaatccc agtccttcag tttgtgcttt tgtgtgtttt 1500

gtttctctga ttacggaat ttggaaataa taagctt                                1537

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<210> 45

<211> 734

<212> DNA

<213> Unknown

<220>

<221> variation

<223> Artificial sequence

<400> 45

ctaacaatca atgagtagag agctggacac atgacggcaa caatggcggc ttttacctgc	60
cctagggttta tgactagcat cagatacacg aagcaaatta agtgcaacgc tgctaaaagc	120
cagctagtcg ttaaacaaga gattgaggag gaagaagatt atgtgaaagc cggtaggatcg	180
gagctgcttt ttgttcaaat gcaacagaat aagtccatgg atgcacagtc tagcctatcc	240
caaaagggtca ctccagactt aattgcttat aaataaataa atatgttttt taggaataat	300
gatattttaga tagattagct atcacctgtg ctgtggtgtg cagctcccaa gggctcttacc	360
gatagtaaaa tcgttagtta tgattaatac ttgggagggtg ggggattata ggctttgttg	420
tgagaatgtt gagaaagagg ttgacaaat cgggtgtttga atgagggtta atggagtta	480
attaaaataa agagaagaga aagattaaga gggtagatggg gatattaaag acggscaata	540
tagtgatgcc acgtagaaaa aggtaagtga aacatacaa cgtggcttta aaagatggct	600
tggttgctaa tcaactcaac tcaactcata tcctatccat tcaaattcaa ttcaattcta	660
ttgaatgcaa agcaaagcaa aggttgtttg ttgttggtgt tgagagacac tccaatccaa	720
acagatacaa ggcg	734

<210> 46

<211> 280

<212> DNA

<213> Unknown

<220>

<221> variation

<223> Artificial sequence

<400> 46

gtcgagtatg gaggttcaatt aaaataaaga gaagaraaag attaagaggg tgatggggat	60
attaaagacg gccaatrtag tgatgccacg taagaaaaag gtaagtgaac acatacaacg	120
tggttttaaa agatggcttg gctgctaata aactcaactc aactcatatc ctatccattc	180

aaattcaatt caattctatt gaatgcaaag caaagcaaag caaaggttgt ttgttgttgt 240
 tgttgagaga cactccaatc caaacagata caaggcgtga 280

<210> 47

<211> 358

<212> DNA

<213> *Tagetes erecta*

<220>

<221> misc_feature

<223> Sense promoter

<400> 47

aagcttaccg atagtaaaat cgtagttat gattaatact tgggaggtgg gggattatag 60
 gctttgttgt gagaatgttg agaaagaggt ttgacaaatc ggtgtttgaa tgagggttaaa 120
 tggagtttaa ttaaaataaa gagaagagaa agattaagag ggtgatgggg atattaaaga 180
 cggccaatat agtgatgcca cgtagaaaaa ggtaagtga aacatacaac gtggctttaa 240
 aagatggctt ggctgctaata caactcaact caactcatat cctatccatt caaattcaat 300
 tcaattctat tgaatgcaaa gcaaagcaaa gcaaaggttg tttgttgttg ttgtcgac 358

<210> 48

<211> 361

<212> DNA

<213> *Tagetes erecta*

<220>

<221> misc_feature

<223> Antisense promoter

<400> 48

ctcgagctta ccgatagtaa aatcgtagt tatgattaat acttgggagg tgggggatta 60
 taggctttgt tgtgagaatg ttgagaaaga ggtttgacaa atcgggtgtt gaatgaggtt 120
 aaatggagtt taattaaaat aaagagaaga gaaagattaa gagggatgat gggatattaa 180
 agacggccaa tatagtgatg ccacgtagaa aaaggtaagt gaaaacatac aacgtggctt 240
 taaaagatgg cttggctgct aatcaactca actcaactca taccctatcc attcaaattc 300
 aattcaattc tattgaatgc aaagcaaagc aaagcaaagg ttgtttgttg ttgttgatc 360

c

361

<210> 49

<211> 28

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 49

gagctcactc actgatttcc attgcttg

28

<210> 50

<211> 37

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 50

cgccgttaag tcgatgtccg ttgatttaaa cagtgtc

37

<210> 51

<211> 34

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 51

atcaacggac atcgacttaa cggcgtttgt aaac

34

<210> 52

<211> 25

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 52

taagcttttt gttgaagaga tttgg

25

<210> 53

<211> 23

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 53

gaaaataactt catcagcatt acc

23

<210> 54

<211> 28

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 54

gtcgactacg taagtttctg cttctacc

28

<210> 55

<211> 26

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 55

ggatccggtg atacctgcac atcaac

26

<210> 56

<211> 28

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 56

aagcttgac gaggcaaagc aaaggttg

28

<210> 57

<211> 29

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 57

gtcgacaacc aaatccagta tacagttac

29

<210> 58

<211> 30

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 58

aggatccaac caaatccagt atacagttac

30

<210> 59

<211> 28

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 59

gaattcgac gaggcaaagc aaaggttg

28

<210> 60

<211> 25

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 60

aagctttgga ttagcactga ttgtc

25

<210> 61

<211> 29

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 61

gtcgacagaa aatacttcat cagcattac

29

<210> 62

<211> 29

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 62

ggatccagaa aatacttcat cagcattac

29

<210> 63

<211> 27

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 63
gaattctctt tggattagca ctgattg

27

<210> 64

<211> 23

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 64
cgccttgat ctgtttggat tgg

23

<210> 65

<211> 24

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 65
ctaacaatca atgagtatga gagc

24

<210> 66

<211> 26

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 66
agagcaaggc cagcaggacc acaacc

26

<210> 67

<211> 26

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 67

ccttgggagc ttttgggata ggctag

26

<210> 68

<211> 26

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 68

tcacgccttg tatctgtttg gattgg

26

<210> 69

<211> 15

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 69

gtcgagtatg gagtt

15

<210> 70

<211> 28

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 70

aagcttaccg atagtaaaat cgttagtt

28

<210> 71

<211> 31

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 71

ctcgagctta ccgatagtaa aatcgtagt t

31

<210> 72

<211> 28

<212> DNA

<213> Unknown

<220>

<223> Artificial sequence

<400> 72

gtcgacaaca acaacaaaca acctttgc

28

<210> 73

<211> 28

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 73

ggatccaaca acaacaaaca acctttgc

28

<210> 74

<211> 28

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 74

gtcgactttt tggtgaagag atttggtg

28

<210> 75

<211> 28

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 75

ctcgagactc actgatttcc attgcttg

28

<210> 76

<211> 22

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 76

gagctctaca aattagggtt ac

22

<210> 77

<211> 23

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 77

aagcttatta tttccaaatt ccg

23

<210> 78

<211> 50

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 78

aagctttgca attcatacag aagtgagaaa aatgcagcta gcagcgacag

50

<210> 79

<211> 1062

<212> DNA

<213> Haematococcus pluvialis

<220>

<221> CDS

<222> (32)..(1021)

<400> 79

aagctttgca attcatacag aagtgagaaa a atg cag cta gca gcg aca gta 52
 Met Gln Leu Ala Ala Thr Val
 1 5

atg ttg gag cag ctt acc gga agc gct gag gca ctc aag gag aag gag 100
 Met Leu Glu Gln Leu Thr Gly Ser Ala Glu Ala Leu Lys Glu Lys Glu
 10 15 20

aag gag gtt gca ggc agc tct gac gtg ttg cgt aca tgg gcg acc cag 148
 Lys Glu Val Ala Gly Ser Ser Asp Val Leu Arg Thr Trp Ala Thr Gln
 25 30 35

tac tcg ctt ccg tca gag gag tca gac gcg gcc cgc ccg gga ctg aag 196
 Tyr Ser Leu Pro Ser Glu Glu Ser Asp Ala Ala Arg Pro Gly Leu Lys
 40 45 50 55

aat gcc tac aag cca cca cct tcc gac aca aag ggc atc aca atg gcg 244
 Asn Ala Tyr Lys Pro Pro Pro Ser Asp Thr Lys Gly Ile Thr Met Ala
 60 65 70

cta gct gtc atc ggc tcc tgg gcc gca gtg ttc ctc cac gcc att ttt 292
 Leu Ala Val Ile Gly Ser Trp Ala Ala Val Phe Leu His Ala Ile Phe
 75 80 85

caa atc aag ctt ccg acc tcc ttg gac cag ctg cac tgg ctg ccc gtg 340
 Gln Ile Lys Leu Pro Thr Ser Leu Asp Gln Leu His Trp Leu Pro Val
 90 95 100

tca gat gcc aca gct cag ctg gtt agc ggc agc agc agc ctg ctg cac 388
 Ser Asp Ala Thr Ala Gln Leu Val Ser Gly Ser Ser Ser Leu Leu His
 105 110 115

atc gtc gta gta ttc ttt gtc ctg gag ttc ctg tac aca ggc ctt ttt 436
 Ile Val Val Val Phe Phe Val Leu Glu Phe Leu Tyr Thr Gly Leu Phe
 120 125 130 135

atc acc acg cat gat gct atg cat ggc acc atc gcc atg aga aac agg 484
 Ile Thr Thr His Asp Ala Met His Gly Thr Ile Ala Met Arg Asn Arg
 140 145 150

cag ctt aat gac ttc ttg ggc aga gta tgc atc tcc ttg tac gcc.tgg 532
 Gln Leu Asn Asp Phe Leu Gly Arg Val Cys Ile Ser Leu Tyr Ala Trp
 155 160 165

ttt gat tac aac atg ctg cac cgc aag cat tgg gag cac cac aac cac 580
 Phe Asp Tyr Asn Met Leu His Arg Lys His Trp Glu His His Asn His
 170 175 180

act ggc gag gtg ggc aag gac cct gac ttc cac agg gga aac cct.ggc 628
 Thr Gly Glu Val Gly Lys Asp Pro Asp Phe His Arg Gly Asn Pro Gly
 185 190 195

att gtg ccc tgg ttt gcc agc ttc atg tcc agc tac atg tcg atg tgg 676
 Ile Val Pro Trp Phe Ala Ser Phe Met Ser Ser Tyr Met Ser Met Trp
 200 205 210 215

cag ttt gcg cgc ctc gca tgg tgg acg gtg gtc atg cag ctg ctg.ggt 724
 Gln Phe Ala Arg Leu Ala Trp Trp Thr Val Val Met Gln Leu Leu Gly
 220 225 230

gcg cca atg gcg aac ctg ctg gtg ttc atg gcg gcc gcg ccc atc.ctg 772
 Ala Pro Met Ala Asn Leu Leu Val Phe Met Ala Ala Ala Pro Ile Leu
 235 240 245

tcc gcc ttc cgc ttg ttc tac ttt ggc acg tac atg ccc cac aag.cct 820
 Ser Ala Phe Arg Leu Phe Tyr Phe Gly Thr Tyr Met Pro His Lys Pro
 250 255 260

gag cct ggc gcc gcg tca ggc tct tca cca gcc gtc atg aac tgg.tgg 868
 Glu Pro Gly Ala Ala Ser Gly Ser Ser Pro Ala Val Met Asn Trp Trp
 265 270 275

aag tcg cgc act agc cag gcg tcc gac ctg gtc agc ttt ctg acc.tgc 916
 Lys Ser Arg Thr Ser Gln Ala Ser Asp Leu Val Ser Phe Leu Thr Cys
 280 285 290 295

tac cac ttc gac ctg cac tgg gag cac cac cgc tgg ccc ttt gcc.ccc 964
 Tyr His Phe Asp Leu His Trp Glu His His Arg Trp Pro Phe Ala Pro
 300 305 310

tgg tgg gag ctg ccc aac tgc cgc cgc ctg tct ggc cga ggt ctg.gtt 1012
 Trp Trp Glu Leu Pro Asn Cys Arg Arg Leu Ser Gly Arg Gly Leu Val
 315 320 325

cct gcc tag ctggacacac tgcagtgggc cctgctgcca gctgggcatg c 1062
 Pro Ala

<210> 80

<211> 329

<212> PRT

<213> Haematococcus pluvialis

<400> 80

Met Gln Leu Ala Ala Thr Val Met Leu Glu Gln Leu Thr Gly Ser Ala

1	5	10	15
Glu Ala Leu Lys Glu Lys Glu Lys Glu Val Ala Gly Ser Ser Asp Val	20	25	30
Leu Arg Thr Trp Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu Ser Asp	35	40	45
Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser Asp	50	55	60
Thr Lys Gly Ile Thr Met Ala Leu Ala Val Ile Gly Ser Trp Ala Ala	65	70	75
Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu Asp	85	90	95
Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val Ser	100	105	110
Gly Ser Ser Ser Leu Leu His Ile Val Val Val Phe Phe Val Leu Glu	115	120	125
Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala Met His Gly	130	135	140
Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg Val	145	150	155
Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg Lys	165	170	175
His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys Asp Pro Asp	180	185	190
Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala Ser Phe Met	195	200	205
Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala Trp Trp Thr	210	215	220
Val Val Met Gln Leu Leu Gly Ala Pro Met Ala Asn Leu Leu Val Phe	225	230	235
Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe Gly			240

245

250

255

Thr Tyr Met Pro His Lys Pro Glu Pro Gly Ala Ala Ser Gly Ser Ser
 260 265 270

Pro Ala Val Met Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser Asp
 275 280 285

Leu Val Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu His
 290 295 300

His Arg Trp Pro Phe Ala Pro Trp Trp Glu Leu Pro Asn Cys Arg Arg
 305 310 315 320

Leu Ser Gly Arg Gly Leu Val Pro Ala
 325

<210> 81

<211> 831

<212> DNA

<213> Haematococcus pluvialis

<220>

<221> CDS

<400> 81

atg cca tcc gag tcg tca gac gca gct cgt cct gtg ttg aag cac gcc 48
 Met Pro Ser Glu Ser Ser Asp Ala Ala Arg Pro Val Leu Lys His Ala
 1 5 10 15

tat aaa cct cca gca tct gac gcc aag ggc atc act atg gcg ctg acc 96
 Tyr Lys Pro Pro Ala Ser Asp Ala Lys Gly Ile Thr Met Ala Leu Thr
 20 25 30

atc att ggc acc tgg acc gca gtg ttt tta cac gca ata ttc caa atc 144
 Ile Ile Gly Thr Trp Thr Ala Val Phe Leu His Ala Ile Phe Gln Ile
 35 40 45

agg cta ccg aca tcc atg gac cag ctt cac tgg ttg cct gtg tcc gaa 192
 Arg Leu Pro Thr Ser Met Asp Gln Leu His Trp Leu Pro Val Ser Glu
 50 55 60

gcc aca gcc cag ctg ttg ggc gga agc agc agc cta ttg cac atc gcc 240
 Ala Thr Ala Gln Leu Leu Gly Gly Ser Ser Ser Leu Leu His Ile Ala
 65 70 75 80

gca gtc ttc att gta ctt gag ttt ctg tac act ggt cta ttc atc acc 288
 Ala Val Phe Ile Val Leu Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr
 85 90 95

acg cat gat gca atg cat ggc acc ata gct ttg agg aac agg cag ctc 336
 Thr His Asp Ala Met His Gly Thr Ile Ala Leu Arg Asn Arg Gln Leu
 100 105 110

aat gat ctc ctt ggc aac atc tgc ata tca ctg tac gcc tgg ttt gac 384
 Asn Asp Leu Leu Gly Asn Ile Cys Ile Ser Leu Tyr Ala Trp Phe Asp
 115 120 125

tac agc atg cac tgg gag cac cac aac cat act ggc gaa gtg ggg aaa 432
 Tyr Ser Met His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys
 130 135 140

gac cct gac ttc cac aaa gga aat cct ggc ctt gtc ccc tgg ttc gcc 480
 Asp Pro Asp Phe His Lys Gly Asn Pro Gly Leu Val Pro Trp Phe Ala
 145 150 155 160

agc ttc atg tcc agc tac atg tcc ctg tgg cag ttt gcc cgg ctg gca 528
 Ser Phe Met Ser Ser Tyr Met Ser Leu Trp Gln Phe Ala Arg Leu Ala
 165 170 175

tgg tgg gca gtg gtg atg caa acg ttg ggg gcc ccc atg gcg aat ctc 576
 Trp Trp Ala Val Val Met Gln Thr Leu Gly Ala Pro Met Ala Asn Leu
 180 185 190

cta gtc ttc atg gct gca gcc cca atc ttg tca gca ttc cgc ctc ttc 624
 Leu Val Phe Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe
 195 200 205

tac ttc ggc act tac ctg cca cac aag cct gag cca ggc cct gca gca 672
 Tyr Phe Gly Thr Tyr Leu Pro His Lys Pro Glu Pro Gly Pro Ala Ala
 210 215 220

ggc tct cag gtc atg tct tgg ttc agg gcc aag aca agt gag gca tct 720
 Gly Ser Gln Val Met Ser Trp Phe Arg Ala Lys Thr Ser Glu Ala Ser
 225 230 235 240

gat gtg atg agc ttc ctg aca tgc tac cac ttt gac ctg ttt gcc ccc 768
 Asp Val Met Ser Phe Leu Thr Cys Tyr His Phe Asp Leu Phe Ala Pro
 245 250 255

tgg tgg cag ctg ccc cac tgc cgc cgc ctg tct ggg cgt ggc ctg gtg 816
 Trp Trp Gln Leu Pro His Cys Arg Arg Leu Ser Gly Arg Gly Leu Val
 260 265 270

cct gcc ttg gca tga 831
 Pro Ala Leu Ala
 275

<210> 82

<211> 276

<212> PRT

<213> Haematococcus pluvialis

<400> 82

Met Pro Ser Glu Ser Ser Asp Ala Ala Arg Pro Val Leu Lys His Ala

1	5	10	15
Tyr Lys Pro Pro Ala Ser Asp Ala Lys Gly Ile Thr Met Ala Leu Thr	20	25	30
Ile Ile Gly Thr Trp Thr Ala Val Phe Leu His Ala Ile Phe Gln Ile	35	40	45
Arg Leu Pro Thr Ser Met Asp Gln Leu His Trp Leu Pro Val Ser Glu	50	55	60
Ala Thr Ala Gln Leu Leu Gly Gly Ser Ser Ser Leu Leu His Ile Ala	65	70	75
Ala Val Phe Ile Val Leu Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr	85	90	95
Thr His Asp Ala Met His Gly Thr Ile Ala Leu Arg Asn Arg Gln Leu	100	105	110
Asn Asp Leu Leu Gly Asn Ile Cys Ile Ser Leu Tyr Ala Trp Phe Asp	115	120	125
Tyr Ser Met His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys	130	135	140
Asp Pro Asp Phe His Lys Gly Asn Pro Gly Leu Val Pro Trp Phe Ala	145	150	155
Ser Phe Met Ser Ser Tyr Met Ser Leu Trp Gln Phe Ala Arg Leu Ala	165	170	175
Trp Trp Ala Val Val Met Gln Thr Leu Gly Ala Pro Met Ala Asn Leu	180	185	190
Leu Val Phe Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe	195	200	205
Tyr Phe Gly Thr Tyr Leu Pro His Lys Pro Glu Pro Gly Pro Ala Ala	210	215	220
Gly Ser Gln Val Met Ser Trp Phe Arg Ala Lys Thr Ser Glu Ala Ser	225	230	235
			240

Asp Val Met Ser Phe Leu Thr Cys Tyr His Phe Asp Leu Phe Ala Pro
 245 250 255

Trp Trp Gln Leu Pro His Cys Arg Arg Leu Ser Gly Arg Gly Leu Val
 260 265 270

Pro Ala Leu Ala
 275

<210> 83

<211> 729

<212> DNA

<213> Paracoccus sp. MBIC1143

<220>

<221> CDS

<400> 83

atg agc gca cat gcc ctg ccc aag gca gat ctg acc gcc acc agc ctg	48
Met Ser Ala His Ala Leu Pro Lys Ala Asp Leu Thr Ala Thr Ser Leu	
1 5 10 15	
atc gtc tcg ggc ggc atc atc gcc gct tgg ctg gcc ctg cat gtg cat	96
Ile Val Ser Gly Gly Ile Ile Ala Ala Trp Leu Ala Leu His Val His	
20 25 30	
gcg ctg tgg ttt ctg gac gca gcg gcg cat ccc atc ctg gcg atc gca	144
Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Ile Ala	
35 40 45	
aat ttc ctg ggg ctg acc tgg ctg tcg gtc gga ttg ttc atc atc gcg	192
Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala	
50 55 60	
cat gac gcg atg cac ggg tcg gtg gtg ccg ggg cgt ccg cgc gcc aat	240
His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn	
65 70 75 80	
gcg gcg atg ggc cag ctt gtc ctg tgg ctg tat gcc gga ttt tcg tgg	288
Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp	
85 90 95	
cgc aag atg atc gtc aag cac atg gcc cat cac cgc cat gcc gga acc	336
Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr	
100 105 110	
gac gac gac ccc gat ttc gac cat ggc ggc ccg gtc cgc tgg tac gcc	384
Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala	
115 120 125	
cgc ttc atc ggc acc tat ttc ggc tgg cgc gag ggg ctg ctg ctg ccc	432
Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro	
130 135 140	

gtc atc gtg acg gtc tat gcg ctg atc ctt ggg gat cgc tgg atg tac 480
 Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr
 145 150 155 160

gtg gtc ttc tgg ccg ctg ccg tcg atc ctg gcg tcg atc cag ctg ttc 528
 Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe
 165 170 175

gtg ttc ggc acc tgg ctg ccg cac cgc ccc ggc cac gac gcg ttc ccg 576
 Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro
 180 185 190

gac cgc cac aat gcg cgg tcg tcg cgg atc agc gac ccc gtg tcg ctg 624
 Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu
 195 200 205

ctg acc tgc ttt cac ttt ggc ggt tat cat cac gaa cac cac ctg cac 672
 Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His
 210 215 220

ccg acg gtg ccg tgg tgg cgc ctg ccc agc acc cgc acc aag ggg gac 720
 Pro Thr Val Pro Trp Trp Arg Leu Pro Ser Thr Arg Thr Lys Gly Asp
 225 230 235 240

acc gca tga 729
 Thr Ala

<210> 84

<211> 242

<212> PRT

<213> Paracoccus sp. MBIC1143

<400> 84

Met Ser Ala His Ala Leu Pro Lys Ala Asp Leu Thr Ala Thr Ser Leu
 1 5 10 15

Ile Val Ser Gly Gly Ile Ile Ala Ala Trp Leu Ala Leu His Val His
 20 25 30

Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Ile Ala
 35 40 45

Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala
 50 55 60

His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn
 65 70 75 80

Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp
85 90 95

Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr
100 105 110

Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala
115 120 125

Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro
130 135 140

Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr
145 150 155 160

Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe
165 170 175

Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro
180 185 190

Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu
195 200 205

Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His
210 215 220

Pro Thr Val Pro Trp Trp Arg Leu Pro Ser Thr Arg Thr Lys Gly Asp
225 230 235 240

Thr Ala

<210> 85

<211> 735

<212> DNA

<213> Brevundimonas aurantiaca

<220>

<221> CDS

<400> 85

atg acc gcc gcc gtc gcc gag cca cgc acc gtc ccg cgc cag acc tgg
Met Thr Ala Ala Val Ala Glu Pro Arg Thr Val Pro Arg Gln Thr Trp
1 5 10 15

atc ggt ctg acc ctg gcg gga atg atc gtg gcg gga tgg gcg gtt ctg Ile Gly Leu Thr Leu Ala Gly Met Ile Val Ala Gly Trp Ala Val Leu 20 25 30	96
cat gtc tac ggc gtc tat ttt cac cga tgg ggg ccg ttg acc ctg gtg His Val Tyr Gly Val Tyr Phe His Arg Trp Gly Pro Leu Thr Leu Val 35 40 45	144
atc gcc ccg gcg atc gtg gcg gtc cag acc tgg ttg tcg gtc ggc ctt Ile Ala Pro Ala Ile Val Ala Val Gln Thr Trp Leu Ser Val Gly Leu 50 55 60	192
ttc atc gtc gcc cat gac gcc atg tac ggc tcc ctg gcg ccg gga cgg Phe Ile Val Ala His Asp Ala Met Tyr Gly Ser Leu Ala Pro Gly Arg 65 70 75 80	240
ccg cgg ctg aac gcc gca gtc ggc cgg ctg acc ctg ggg ctc tat gcg Pro Arg Leu Asn Ala Ala Val Gly Arg Leu Thr Leu Gly Leu Tyr Ala 85 90 95	288
ggc ttc cgc ttc gat cgg ctg aag acg gcg cac cac gcc cac cac gcc Gly Phe Arg Phe Asp Arg Leu Lys Thr Ala His His Ala His His Ala 100 105 110	336
gcg ccc ggc acg gcc gac gac ccg gat ttt cac gcc ccg gcg ccc cgc Ala Pro Gly Thr Ala Asp Asp Pro Asp Phe His Ala Pro Ala Pro Arg 115 120 125	384
gcc ttc ctt ccc tgg ttc ctg aac ttc ttt cgc acc tat ttc ggc tgg Ala Phe Leu Pro Trp Phe Leu Asn Phe Phe Arg Thr Tyr Phe Gly Trp 130 135 140	432
cgc gag atg gcg gtc ctg acc gcc ctg gtc ctg atc gcc ctc ttc ggc Arg Glu Met Ala Val Leu Thr Ala Leu Val Leu Ile Ala Leu Phe Gly 145 150 155 160	480
ctg ggg gcg cgg ccg gcc aat ctc ctg acc ttc tgg gcc gcg ccg gcc Leu Gly Ala Arg Pro Ala Asn Leu Leu Thr Phe Trp Ala Ala Pro Ala 165 170 175	528
ctg ctt tca gcg ctt cag ctc ttc acc ttc ggc acc tgg ctg ccg cac Leu Leu Ser Ala Leu Gln Leu Phe Thr Phe Gly Thr Trp Leu Pro His 180 185 190	576
cgc cac acc gac cag ccg ttc gcc gac gcg cac cac gcc cgc agc agc Arg His Thr Asp Gln Pro Phe Ala Asp Ala His His Ala Arg Ser Ser 195 200 205	624
ggc tac ggc ccc gtg ctt tcc ctg ctc acc tgt ttc cac ttc ggc cgc Gly Tyr Gly Pro Val Leu Ser Leu Leu Thr Cys Phe His Phe Gly Arg 210 215 220	672
cac cac gaa cac cat ctg agc ccc tgg cgg ccc tgg tgg cgt ctg tgg His His Glu His His Leu Ser Pro Trp Arg Pro Trp Trp Arg Leu Trp 225 230 235 240	720
cgc ggc gag tct tga Arg Gly Glu Ser	735

<210> 86

<211> 244

<212> PRT

<213> Brevundimonas aurantiaca

<400> 86

Met Thr Ala Ala Val Ala Glu Pro Arg Thr Val Pro Arg Gln Thr Trp
 1 5 10 15

Ile Gly Leu Thr Leu Ala Gly Met Ile Val Ala Gly Trp Ala Val Leu
 20 25 30

His Val Tyr Gly Val Tyr Phe His Arg Trp Gly Pro Leu Thr Leu Val
 35 40 45

Ile Ala Pro Ala Ile Val Ala Val Gln Thr Trp Leu Ser Val Gly Leu
 50 55 60

Phe Ile Val Ala His Asp Ala Met Tyr Gly Ser Leu Ala Pro Gly Arg
 65 70 75 80

Pro Arg Leu Asn Ala Ala Val Gly Arg Leu Thr Leu Gly Leu Tyr Ala
 85 90 95

Gly Phe Arg Phe Asp Arg Leu Lys Thr Ala His His Ala His His Ala
 100 105 110

Ala Pro Gly Thr Ala Asp Asp Pro Asp Phe His Ala Pro Ala Pro Arg
 115 120 125

Ala Phe Leu Pro Trp Phe Leu Asn Phe Phe Arg Thr Tyr Phe Gly Trp
 130 135 140

Arg Glu Met Ala Val Leu Thr Ala Leu Val Leu Ile Ala Leu Phe Gly
 145 150 155 160

Leu Gly Ala Arg Pro Ala Asn Leu Leu Thr Phe Trp Ala Ala Pro Ala
 165 170 175

Leu Leu Ser Ala Leu Gln Leu Phe Thr Phe Gly Thr Trp Leu Pro His
 180 185 190

Arg His Thr Asp Gln Pro Phe Ala Asp Ala His His Ala Arg Ser Ser
 195 200 205

Gly Tyr Gly Pro Val Leu Ser Leu Leu Thr Cys Phe His Phe Gly Arg
 210 215 220

His His Glu His His Leu Ser Pro Trp Arg Pro Trp Trp Arg Leu Trp
 225 230 235 240

Arg Gly Glu Ser

<210> 87

<211> 690

<212> DNA

<213> Nodularia spumigena NSOR10

<220>

<221> CDS

<400> 87

atg gcg atc gcc att att agt ata tgg gct atc agc cta ggt ttg tta	48
Met Ala Ile Ala Ile Ile Ser Ile Trp Ala Ile Ser Leu Gly Leu Leu	
1 5 10 15	
ctt tat att gat ata tcc caa ttc aag ttt tgg atg ttg tta ccg ctc	96
Leu Tyr Ile Asp Ile Ser Gln Phe Lys Phe Trp Met Leu Leu Pro Leu	
20 25 30	
ata ttt tgg caa aca ttt tta tat acg gga tta ttt att aca gct cat	144
Ile Phe Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His	
35 40 45	
gat gcc atg cat ggg gta gtt ttt ccc aaa aat ccc aaa atc aac cat	192
Asp Ala Met His Gly Val Val Phe Pro Lys Asn Pro Lys Ile Asn His	
50 55 60	
ttc att ggc tca ttg tgc ctg ttt ctt tat ggt ctt tta cct tat caa	240
Phe Ile Gly Ser Leu Cys Leu Phe Leu Tyr Gly Leu Leu Pro Tyr Gln	
65 70 75 80	
aaa ctt tta aaa aag cat tgg cta cat cac cat aat cca gcc agt gaa	288
Lys Leu Leu Lys Lys His Trp Leu His His His Asn Pro Ala Ser Glu	
85 90 95	
aca gat cca gat ttt cac aac ggg aag cag aaa aac ttt ttt gct tgg	336
Thr Asp Pro Asp Phe His Asn Gly Lys Gln Lys Asn Phe Phe Ala Trp	
100 105 110	
tat tta tat ttt atg aag cgt tac tgg agt tgg tta caa att atc aca	384
Tyr Leu Tyr Phe Met Lys Arg Tyr Trp Ser Trp Leu Gln Ile Ile Thr	
115 120 125	

tta atg att att tat aac tta cta aaa tat ata tgg cat ttt cca gag 432
 Leu Met Ile Ile Tyr Asn Leu Leu Lys Tyr Ile Trp His Phe Pro Glu
 130 135 140

gat aat atg act tat ttt tgg gta gtt ccc tca att tta agt tct tta 480
 Asp Asn Met Thr Tyr Phe Trp Val Val Pro Ser Ile Leu Ser Ser Leu
 145 150 155 160

caa tta ttt tat ttt gga act ttt cta ccc cac agt gag cct gta gaa 528
 Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Ser Glu Pro Val Glu
 165 170 175

ggt tat aaa gag cct cat cgt tcc caa act att agc cgt ccc att tgg 576
 Gly Tyr Lys Glu Pro His Arg Ser Gln Thr Ile Ser Arg Pro Ile Trp
 180 185 190

tgg tca ttt ata act tgt tac cat ttt ggt tat cat tac gaa cat cat 624
 Trp Ser Phe Ile Thr Cys Tyr His Phe Gly Tyr His Tyr Glu His His
 195 200 205

gaa tac ccc cat gtt cct tgg tgg caa tta cca gaa att tat aaa atg 672
 Glu Tyr Pro His Val Pro Trp Trp Gln Leu Pro Glu Ile Tyr Lys Met
 210 215 220

tct aaa tca aat ttg tga 690
 Ser Lys Ser Asn Leu
 225

<210> 88

<211> 229

<212> PRT

<213> Nodularia spumigena NSOR10

<400> 88

Met Ala Ile Ala Ile Ile Ser Ile Trp Ala Ile Ser Leu Gly Leu Leu
 1 5 10 15

Leu Tyr Ile Asp Ile Ser Gln Phe Lys Phe Trp Met Leu Leu Pro Leu
 20 25 30

Ile Phe Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His
 35 40 45

Asp Ala Met His Gly Val Val Phe Pro Lys Asn Pro Lys Ile Asn His
 50 55 60

Phe Ile Gly Ser Leu Cys Leu Phe Leu Tyr Gly Leu Leu Pro Tyr Gln
 65 70 75 80

Lys Leu Leu Lys Lys His Trp Leu His His His Asn Pro Ala Ser Glu
85 90 95

Thr Asp Pro Asp Phe His Asn Gly Lys Gln Lys Asn Phe Phe Ala Trp
100 105 110

Tyr Leu Tyr Phe Met Lys Arg Tyr Trp Ser Trp Leu Gln Ile Ile Thr
115 120 125

Leu Met Ile Ile Tyr Asn Leu Leu Lys Tyr Ile Trp His Phe Pro Glu
130 135 140

Asp Asn Met Thr Tyr Phe Trp Val Val Pro Ser Ile Leu Ser Ser Leu
145 150 155 160

Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Ser Glu Pro Val Glu
165 170 175

Gly Tyr Lys Glu Pro His Arg Ser Gln Thr Ile Ser Arg Pro Ile Trp
180 185 190

Trp Ser Phe Ile Thr Cys Tyr His Phe Gly Tyr His Tyr Glu His His
195 200 205

Glu Tyr Pro His Val Pro Trp Trp Gln Leu Pro Glu Ile Tyr Lys Met
210 215 220

Ser Lys Ser Asn Leu
225

<210> 89

<211> 789

<212> DNA

<213> Nostoc punctiforme ATCC 29133

<220>

<221> CDS

<400> 89

ttg aat ttt tgt gat aaa cca gtt agc tat tat gtt gca ata gag caa 48
Leu Asn Phe Cys Asp Lys Pro Val Ser Tyr Tyr Val Ala Ile Glu Gln
1 5 10 15

tta agt gct aaa gaa gat act gtt tgg ggg ctg gtg att gtc ata gta 96
Leu Ser Ala Lys Glu Asp Thr Val Trp Gly Leu Val Ile Val Ile Val
20 25 30

att att agt ctt tgg gta gct agt ttg gct ttt tta cta gct att aat Ile Ile Ser Leu Trp Val Ala Ser Leu Ala Phe Leu Leu Ala Ile Asn 35 40 45	144
tat gcc aaa gtc cca att tgg ttg ata cct att gca ata gtt tgg caa Tyr Ala Lys Val Pro Ile Trp Leu Ile Pro Ile Ala Ile Val Trp Gln 50 55 60	192
atg ttc ctt tat aca ggg cta ttt att act gca cat gat gct atg cat Met Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His Asp Ala Met His 65 70 75 80	240
ggg tca gtt tat cgt aaa aat ccc aaa att aat aat ttt atc ggt tca Gly Ser Val Tyr Arg Lys Asn Pro Lys Ile Asn Asn Phe Ile Gly Ser 85 90 95	288
cta gct gta gcg ctt tac gct gtg ttt cca tat caa cag atg tta aag Leu Ala Val Ala Leu Tyr Ala Val Phe Pro Tyr Gln Gln Met Leu Lys 100 105 110	336
aat cat tgc tta cat cat cgt cat cct gct agc gaa gtt gac cca gat Asn His Cys Leu His His Arg His Pro Ala Ser Glu Val Asp Pro Asp 115 120 125	384
ttt cat gat ggt aag aga aca aac gct att ttc tgg tat ctc cat ttc Phe His Asp Gly Lys Arg Thr Asn Ala Ile Phe Trp Tyr Leu His Phe 130 135 140	432
atg ata gaa tac tcc agt tgg caa cag tta ata gta cta act atc cta Met Ile Glu Tyr Ser Ser Trp Gln Gln Leu Ile Val Leu Thr Ile Leu 145 150 155 160	480
ttt aat tta gct aaa tac gtt ttg cac atc cat caa ata aat ctc atc Phe Asn Leu Ala Lys Tyr Val Leu His Ile His Gln Ile Asn Leu Ile 165 170 175	528
tta ttt tgg agt att cct cca att tta agt tcc att caa ctg ttt tat Leu Phe Trp Ser Ile Pro Pro Ile Leu Ser Ser Ile Gln Leu Phe Tyr 180 185 190	576
ttc gga aca ttt ttg cct cat cga gaa ccc aag aaa gga tat gtt tat Phe Gly Thr Phe Leu Pro His Arg Glu Pro Lys Lys Gly Tyr Val Tyr 195 200 205	624
ccc cat tgc agc caa aca ata aaa ttg cca act ttt ttg tca ttt atc Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr Phe Leu Ser Phe Ile 210 215 220	672
gct tgc tac cac ttt ggt tat cat gaa gaa cat cat gag tat ccc cat Ala Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His 225 230 235 240	720
gta cct tgg tgg caa ctt cca tct gta tat aag cag aga gta ttc aac Val Pro Trp Trp Gln Leu Pro Ser Val Tyr Lys Gln Arg Val Phe Asn 245 250 255	768
aat tca gta acc aat tcg taa Asn Ser Val Thr Asn Ser 260	789

<210> 90

<211> 262

<212> PRT

<213> Nostoc punctiforme ATCC 29133

<400> 90

Leu Asn Phe Cys Asp Lys Pro Val Ser Tyr Tyr Val Ala Ile Glu Gln
1 5 10 15

Leu Ser Ala Lys Glu Asp Thr Val Trp Gly Leu Val Ile Val Ile Val
20 25 30

Ile Ile Ser Leu Trp Val Ala Ser Leu Ala Phe Leu Leu Ala Ile Asn
35 40 45

Tyr Ala Lys Val Pro Ile Trp Leu Ile Pro Ile Ala Ile Val Trp Gln
50 55 60

Met Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His Asp Ala Met His
65 70 75 80

Gly Ser Val Tyr Arg Lys Asn Pro Lys Ile Asn Asn Phe Ile Gly Ser
85 90 95

Leu Ala Val Ala Leu Tyr Ala Val Phe Pro Tyr Gln Gln Met Leu Lys
100 105 110

Asn His Cys Leu His His Arg His Pro Ala Ser Glu Val Asp Pro Asp
115 120 125

Phe His Asp Gly Lys Arg Thr Asn Ala Ile Phe Trp Tyr Leu His Phe
130 135 140

Met Ile Glu Tyr Ser Ser Trp Gln Gln Leu Ile Val Leu Thr Ile Leu
145 150 155 160

Phe Asn Leu Ala Lys Tyr Val Leu His Ile His Gln Ile Asn Leu Ile
165 170 175

Leu Phe Trp Ser Ile Pro Pro Ile Leu Ser Ser Ile Gln Leu Phe Tyr
180 185 190

Phe Gly Thr Phe Leu Pro His Arg Glu Pro Lys Lys Gly Tyr Val Tyr
 195 200 205

Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr Phe Leu Ser Phe Ile
 210 215 220

Ala Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His
 225 230 235 240

Val Pro Trp Trp Gln Leu Pro Ser Val Tyr Lys Gln Arg Val Phe Asn
 245 250 255

Asn Ser Val Thr Asn Ser
 260

<210> 91

<211> 762

<212> DNA

<213> Nostoc punctiforme ATCC 29133

<220>

<221> CDS

<400> 91

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 Val Ile Gln Leu Glu Gln Pro Leu Ser His Gln Ala Lys Leu Thr Pro
 1 5 10 15

gta ctg aga agt aaa tct cag ttt aag ggg ctt ttc att gct att gtc 96
 Val Leu Arg Ser Lys Ser Gln Phe Lys Gly Leu Phe Ile Ala Ile Val
 20 25 30

att gtt agc gca tgg gtc att agc ctg agt tta tta ctt tcc ctt gac 144
 Ile Val Ser Ala Trp Val Ile Ser Leu Ser Leu Leu Ser Leu Asp
 35 40 45

atc tca aag cta aaa ttt tgg atg tta ttg cct gtt ata cta tgg caa 192
 Ile Ser Lys Leu Lys Phe Trp Met Leu Leu Pro Val Ile Leu Trp Gln
 50 55 60

aca ttt tta tat acg gga tta ttt att aca tct cat gat gcc atg cat 240
 Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser His Asp Ala Met His
 65 70 75 80

ggc gta gta ttt ccc caa aac acc aag att aat cat ttg att gga aca 288
 Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn His Leu Ile Gly Thr
 85 90 95

ttg acc cta tcc ctt tat ggt ctt tta cca tat caa aaa cta ttg aaa 336
 Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr Gln Lys Leu Leu Lys

100	105	110	
aaa cat tgg tta cac cac cac aat cca gca agc tca ata gac ccg gat			384
Lys His Trp Leu His His His Asn Pro Ala Ser Ser Ile Asp Pro Asp			
115	120	125	
ttt cac aat ggt aaa cac caa agt ttc ttt gct tgg tat ttt cat ttt			432
Phe His Asn Gly Lys His Gln Ser Phe Phe Ala Trp Tyr Phe His Phe			
130	135	140	
atg aaa ggt tac tgg agt tgg ggg caa ata att gcg ttg act att att			480
Met Lys Gly Tyr Trp Ser Trp Gly Gln Ile Ile Ala Leu Thr Ile Ile			
145	150	155	160
tat aac ttt gct aaa tac ata ctc cat atc cca agt gat aat cta act			528
Tyr Asn Phe Ala Lys Tyr Ile Leu His Ile Pro Ser Asp Asn Leu Thr			
165	170	175	
tac ttt tgg gtg cta ccc tcg ctt tta agt tca tta caa tta ttc tat			576
Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser Leu Gln Leu Phe Tyr			
180	185	190	
ttt ggt act ttt tta ccc cat agt gaa cca ata ggg ggt tat gtt cag			624
Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile Gly Gly Tyr Val Gln			
195	200	205	
cct cat tgt gcc caa aca att agc cgt cct att tgg tgg tca ttt atc			672
Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile Trp Trp Ser Phe Ile			
210	215	220	
acg tgc tat cat ttt ggc tac cac gag gaa cat cac gaa tat cct cat			720
Thr Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His			
225	230	235	240
att tct tgg tgg cag tta cca gaa att tac aaa gca aaa tag			762
Ile Ser Trp Trp Gln Leu Pro Glu Ile Tyr Lys Ala Lys			
245	250		

<210> 92

<211> 253

<212> PRT

<213> Nostoc punctiforme ATCC 29133

<400> 92

Val Ile Gln Leu Glu Gln Pro Leu Ser His Gln Ala Lys Leu Thr Pro
1 5 10 15

Val Leu Arg Ser Lys Ser Gln Phe Lys Gly Leu Phe Ile Ala Ile Val
20 25 30

Ile Val Ser Ala Trp Val Ile Ser Leu Ser Leu Leu Leu Ser Leu Asp
35 40 45

Ile Ser Lys Leu Lys Phe Trp Met Leu Leu Pro Val Ile Leu Trp Gln
 50 55 60

Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser His Asp Ala Met His
 65 70 75 80

Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn His Leu Ile Gly Thr
 85 90 95

Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr Gln Lys Leu Leu Lys
 100 105 110

Lys His Trp Leu His His His Asn Pro Ala Ser Ser Ile Asp Pro Asp
 115 120 125

Phe His Asn Gly Lys His Gln Ser Phe Phe Ala Trp Tyr Phe His Phe
 130 135 140

Met Lys Gly Tyr Trp Ser Trp Gly Gln Ile Ile Ala Leu Thr Ile Ile
 145 150 155 160

Tyr Asn Phe Ala Lys Tyr Ile Leu His Ile Pro Ser Asp Asn Leu Thr
 165 170 175

Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser Leu Gln Leu Phe Tyr
 180 185 190

Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile Gly Gly Tyr Val Gln
 195 200 205

Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile Trp Trp Ser Phe Ile
 210 215 220

Thr Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His
 225 230 235 240

Ile Ser Trp Trp Gln Leu Pro Glu Ile Tyr Lys Ala Lys
 245 250

<210> 93

<211> 1536

<212> DNA

<213> Deinococcus radiodurans R1

<220>

<221> CDS

<400> 93

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Met Pro Asp Tyr Asp Leu Ile Val Met Gly Ala Gly His Asn Ala Leu	
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gtg act gct gcc tac gcc gcc cgg gcg ggc ctg aaa gtc ggc gtg ttc	96
Val Thr Ala Ala Tyr Ala Ala Arg Ala Gly Leu Lys Val Gly Val Phe	
20 25 30	
gag cgg cgg cac ctc gtc ggc ggg gcg gtc agc acc gag gag gtc gtg	144
Glu Arg Arg His Leu Val Gly Gly Ala Val Ser Thr Glu Glu Val Val	
35 40 45	
ccc ggt tac cgc ttc gac tac ggc ggc agc gcc cac atc ctg att cgg	192
Pro Gly Tyr Arg Phe Asp Tyr Gly Gly Ser Ala His Ile Leu Ile Arg	
50 55 60	
atg acg ccc atc gtg cgc gaa ctc gaa ctc acg cgg cac ggg ctg cat	240
Met Thr Pro Ile Val Arg Glu Leu Glu Leu Thr Arg His Gly Leu His	
65 70 75 80	
tac ctc gaa gtg gac cct atg ttt cac gct tcc gac ggt gaa acg ccc	288
Tyr Leu Glu Val Asp Pro Met Phe His Ala Ser Asp Gly Glu Thr Pro	
85 90 95	
tgg ttc att cac cgc gac gcc ggg cgg acc atc cgc gaa ctg gac gaa	336
Trp Phe Ile His Arg Asp Ala Gly Arg Thr Ile Arg Glu Leu Asp Glu	
100 105 110	
aag ttt ccc ggg cag ggc gac gcc tac ggg cgc ttt ctc gac gat tgg	384
Lys Phe Pro Gly Gln Gly Asp Ala Tyr Gly Arg Phe Leu Asp Asp Trp	
115 120 125	
aca ccc ttc gcg cgc gcc gtg gcc gac ctg ttc aac tcg gcg ccg ggg	432
Thr Pro Phe Ala Arg Ala Val Ala Asp Leu Phe Asn Ser Ala Pro Gly	
130 135 140	
ccg ctc gac ctg ggc aaa atg gtg atg cgc agc ggc cag ggc aag gac	480
Pro Leu Asp Leu Gly Lys Met Val Met Arg Ser Gly Gln Gly Lys Asp	
145 150 155 160	
tgg aac gag cag ctc ccg cgc atc ctg cgg ccc tac ggc gac gtg gcg	528
Trp Asn Glu Gln Leu Pro Arg Ile Leu Arg Pro Tyr Gly Asp Val Ala	
165 170 175	
cgc gag tac ttc agc gag gag cgc gtg cgg gct ccc ctg acc tgg atg	576
Arg Glu Tyr Phe Ser Glu Glu Arg Val Arg Ala Pro Leu Thr Trp Met	
180 185 190	
gcg gcc cag agc ggc ccc cca ccc tcg gac ccg ctg agc gcg ccc ttt	624
Ala Ala Gln Ser Gly Pro Pro Pro Ser Asp Pro Leu Ser Ala Pro Phe	
195 200 205	
ttg ctg tgg cac ccg ctc tac cac gaa ggc ggc gtg gcg cgg ccc aaa	672
Leu Leu Trp His Pro Leu Tyr His Glu Gly Gly Val Ala Arg Pro Lys	

210	215	220	
ggc ggc agc ggc ggc ctg acc aaa gcc ctg cgc cgg gcc acc gag gcc Gly Gly Ser Gly Gly Leu Thr Lys Ala Leu Arg Arg Ala Thr Glu Ala 225 230 235 240			720
gaa ggc ggc gag gtc ttc acc gac gcg ccg gtc aag gaa att ctg gtc Glu Gly Gly Glu Val Phe Thr Asp Ala Pro Val Lys Glu Ile Leu Val 245 250 255			768
aag gac ggc aag gcg cag ggc atc cgg ctg gaa agc ggc gag acg tac Lys Asp Gly Lys Ala Gln Gly Ile Arg Leu Glu Ser Gly Glu Thr Tyr 260 265 270			816
acc gcc cgc gcc gtc gtg tcg ggc gtc cac atc ctg acc act gcg aat Thr Ala Arg Ala Val Val Ser Gly Val His Ile Leu Thr Thr Ala Asn 275 280 285			864
gcc ctg ccc gcc gaa tat gtc cct agc gcc gcc agg aat gtg cgc gtg Ala Leu Pro Ala Glu Tyr Val Pro Ser Ala Ala Arg Asn Val Arg Val 290 295 300			912
ggc aac ggc ttc ggc atg att ttg cgc ctc gcc ctc agt gaa aaa gtc Gly Asn Gly Phe Gly Met Ile Leu Arg Leu Ala Leu Ser Glu Lys Val 305 310 315 320			960
aaa tac cgt cac cac acc gag ccc gac tca cgc atc ggc ctg gga ttg Lys Tyr Arg His His Thr Glu Pro Asp Ser Arg Ile Gly Leu Gly Leu 325 330 335			1008
ctg atc aaa aac gag cgg caa atc atg cag ggc tac ggc gaa tac ctc Leu Ile Lys Asn Glu Arg Gln Ile Met Gln Gly Tyr Gly Glu Tyr Leu 340 345 350			1056
gcc ggc cag ccc acc acc gac ccg ccc ctc gtc gcc atg agc ttc agc Ala Gly Gln Pro Thr Thr Asp Pro Pro Leu Val Ala Met Ser Phe Ser 355 360 365			1104
gcg gtg gac gac tcg ctc gcc cca ccg aac ggc gac gtg ttg tgg ctg Ala Val Asp Asp Ser Leu Ala Pro Pro Asn Gly Asp Val Leu Trp Leu 370 375 380			1152
tgg gcg cag tac tac ccc ttc gag ctc gcc acc ggc agc tgg gaa acg Trp Ala Gln Tyr Tyr Pro Phe Glu Leu Ala Thr Gly Ser Trp Glu Thr 385 390 395 400			1200
cgc acc gcc gaa gcg cgg gag aac atc ctg cgg gcc ttt gag cac tac Arg Thr Ala Glu Ala Arg Glu Asn Ile Leu Arg Ala Phe Glu His Tyr 405 410 415			1248
gcg ccg ggc acc cgc gac acg att gtg ggc gaa ctc gtg cag acg ccg Ala Pro Gly Thr Arg Asp Thr Ile Val Gly Glu Leu Val Gln Thr Pro 420 425 430			1296
cag tgg ctg gaa acc aac ctc ggc ctg cac cgg ggc aac gtg atg cac Gln Trp Leu Glu Thr Asn Leu Gly Leu His Arg Gly Asn Val Met His 435 440 445			1344
ctg gaa atg tcc ttc gac cag atg ttc tcc ttc cgc ccc tgg ctg aaa Leu Glu Met Ser Phe Asp Gln Met Phe Ser Phe Arg Pro Trp Leu Lys			1392

450	455	460	
gcg agc cag tac cgc tgg ccg ggc gtg cag ggg ctg tac ctc acc ggc			1440
Ala Ser Gln Tyr Arg Trp Pro Gly Val Gln Gly Leu Tyr Leu Thr Gly			
465	470	475	480
gcc agc acc cac ccc ggc gga ggc atc atg ggc gcc tcg gga cgc aac			1488
Ala Ser Thr His Pro Gly Gly Gly Ile Met Gly Ala Ser Gly Arg Asn			
	485	490	495
gcg gcg cgg gtc atc gtg aag gac ctg acg cgg agg cgc tgg aaa tga			1536
Ala Ala Arg Val Ile Val Lys Asp Leu Thr Arg Arg Arg Trp Lys			
	500	505	510
<210> 94			
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<213> Deinococcus radiodurans R1			
<400> 94			
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1	5	10	15
Val Thr Ala Ala Tyr Ala Ala Arg Ala Gly Leu Lys Val Gly Val Phe			
	20	25	30
Glu Arg Arg His Leu Val Gly Gly Ala Val Ser Thr Glu Glu Val Val			
	35	40	45
Pro Gly Tyr Arg Phe Asp Tyr Gly Gly Ser Ala His Ile Leu Ile Arg			
	50	55	60
Met Thr Pro Ile Val Arg Glu Leu Glu Leu Thr Arg His Gly Leu His			
65	70	75	80
Tyr Leu Glu Val Asp Pro Met Phe His Ala Ser Asp Gly Glu Thr Pro			
	85	90	95
Trp Phe Ile His Arg Asp Ala Gly Arg Thr Ile Arg Glu Leu Asp Glu			
	100	105	110
Lys Phe Pro Gly Gln Gly Asp Ala Tyr Gly Arg Phe Leu Asp Asp Trp			
	115	120	125
Thr Pro Phe Ala Arg Ala Val Ala Asp Leu Phe Asn Ser Ala Pro Gly			
	130	135	140

Pro Leu Asp Leu Gly Lys Met Val Met Arg Ser Gly Gln Gly Lys Asp
145 150 155 160

Trp Asn Glu Gln Leu Pro Arg Ile Leu Arg Pro Tyr Gly Asp Val Ala
165 170 175

Arg Glu Tyr Phe Ser Glu Glu Arg Val Arg Ala Pro Leu Thr Trp Met
180 185 190

Ala Ala Gln Ser Gly Pro Pro Pro Ser Asp Pro Leu Ser Ala Pro Phe
195 200 205

Leu Leu Trp His Pro Leu Tyr His Glu Gly Gly Val Ala Arg Pro Lys
210 215 220

Gly Gly Ser Gly Gly Leu Thr Lys Ala Leu Arg Arg Ala Thr Glu Ala
225 230 235 240

Glu Gly Gly Glu Val Phe Thr Asp Ala Pro Val Lys Glu Ile Leu Val
245 250 255

Lys Asp Gly Lys Ala Gln Gly Ile Arg Leu Glu Ser Gly Glu Thr Tyr
260 265 270

Thr Ala Arg Ala Val Val Ser Gly Val His Ile Leu Thr Thr Ala Asn
275 280 285

Ala Leu Pro Ala Glu Tyr Val Pro Ser Ala Ala Arg Asn Val Arg Val
290 295 300

Gly Asn Gly Phe Gly Met Ile Leu Arg Leu Ala Leu Ser Glu Lys Val
305 310 315 320

Lys Tyr Arg His His Thr Glu Pro Asp Ser Arg Ile Gly Leu Gly Leu
325 330 335

Leu Ile Lys Asn Glu Arg Gln Ile Met Gln Gly Tyr Gly Glu Tyr Leu
340 345 350

Ala Gly Gln Pro Thr Thr Asp Pro Pro Leu Val Ala Met Ser Phe Ser
355 360 365

Ala Val Asp Asp Ser Leu Ala Pro Pro Asn Gly Asp Val Leu Trp Leu
370 375 380

Trp Ala Gln Tyr Tyr Pro Phe Glu Leu Ala Thr Gly Ser Trp Glu Thr
385 390 395 400

Arg Thr Ala Glu Ala Arg Glu Asn Ile Leu Arg Ala Phe Glu His Tyr
405 410 415

Ala Pro Gly Thr Arg Asp Thr Ile Val Gly Glu Leu Val Gln Thr Pro
420 425 430

Gln Trp Leu Glu Thr Asn Leu Gly Leu His Arg Gly Asn Val Met His
435 440 445

Leu Glu Met Ser Phe Asp Gln Met Phe Ser Phe Arg Pro Trp Leu Lys
450 455 460

Ala Ser Gln Tyr Arg Trp Pro Gly Val Gln Gly Leu Tyr Leu Thr Gly
465 470 475 480

Ala Ser Thr His Pro Gly Gly Gly Ile Met Gly Ala Ser Gly Arg Asn
485 490 495

Ala Ala Arg Val Ile Val Lys Asp Leu Thr Arg Arg Arg Trp Lys
500 505 510

<210> 95

<211> 1666

<212> DNA

<213> Lycopersicon esculentum

<220>

<221> CDS

<222> (1)..(1494)

<400> 95

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Met Glu Ala Leu Leu Lys Pro Phe Pro Ser Leu Leu Leu Ser Ser Pro
1 5 10 15

aca ccc cat agg tct att ttc caa caa aat ccc tct ttt cta agt ccc 96
Thr Pro His Arg Ser Ile Phe Gln Gln Asn Pro Ser Phe Leu Ser Pro
20 25 30

acc acc aaa aaa aaa tca aga aaa tgt ctt ctt aga aac aaa agt agt 144
Thr Thr Lys Lys Lys Ser Arg Lys Cys Leu Leu Arg Asn Lys Ser Ser

35	40	45	
aaa ctt ttt tgt agc ttt ctt gat tta gca ccc aca tca aag cca gag Lys Leu Phe Cys Ser Phe Leu Asp Leu Ala Pro Thr Ser Lys Pro Glu 50 55 60			192
tct tta gat gtt aac atc tca tgg gtt gat cct aat tcg aat cgg gct Ser Leu Asp Val Asn Ile Ser Trp Val Asp Pro Asn Ser Asn Arg Ala 65 70 75 80			240
caa ttc gac gtg atc att atc gga gct ggc cct gct ggg ctc agg cta Gln Phe Asp Val Ile Ile Ile Gly Ala Gly Pro Ala Gly Leu Arg Leu 85 90 95			288
gct gaa caa gtt tct aaa tat ggt att aag gta tgt tgt gtt gac cct Ala Glu Gln Val Ser Lys Tyr Gly Ile Lys Val Cys Cys Val Asp Pro 100 105 110			336
tca cca ctc tcc atg tgg cca aat aat tat ggt gtt tgg gtt gat gag Ser Pro Leu Ser Met Trp Pro Asn Asn Tyr Gly Val Trp Val Asp Glu 115 120 125			384
ttt gag aat tta gga ctg gaa aat tgt tta gat cat aaa tgg cct atg Phe Glu Asn Leu Gly Leu Glu Asn Cys Leu Asp His Lys Trp Pro Met 130 135 140			432
act tgt gtg cat ata aat gat aac aaa act aag tat ttg gga aga cca Thr Cys Val His Ile Asn Asp Asn Lys Thr Lys Tyr Leu Gly Arg Pro 145 150 155 160			480
tat ggt aga gtt agt aga aag aag ctg aag ttg aaa ttg ttg aat agt Tyr Gly Arg Val Ser Arg Lys Lys Leu Lys Leu Lys Leu Leu Asn Ser 165 170 175			528
tgt gtt gag aac aga gtg aag ttt tat aaa gct aag gtt tgg aaa gtg Cys Val Glu Asn Arg Val Lys Phe Tyr Lys Ala Lys Val Trp Lys Val 180 185 190			576
gaa cat gaa gaa ttt gag tct tca att gtt tgt gat gat ggt aag aag Glu His Glu Glu Phe Glu Ser Ser Ile Val Cys Asp Asp Gly Lys Lys 195 200 205			624
ata aga ggt agt ttg gtt gtg gat gca agt ggt ttt gct agt gat ttt Ile Arg Gly Ser Leu Val Val Asp Ala Ser Gly Phe Ala Ser Asp Phe 210 215 220			672
ata gag tat gac agg cca aga aac cat ggt tat caa att gct cat ggg Ile Glu Tyr Asp Arg Pro Arg Asn His Gly Tyr Gln Ile Ala His Gly 225 230 235 240			720
gtt tta gta gaa gtt gat aat cat cca ttt gat ttg gat aaa atg gtg Val Leu Val Glu Val Asp Asn His Pro Phe Asp Leu Asp Lys Met Val 245 250 255			768
ctt atg gat tgg agg gat tct cat ttg ggt aat gag cca tat tta agg Leu Met Asp Trp Arg Asp Ser His Leu Gly Asn Glu Pro Tyr Leu Arg 260 265 270			816
gtg aat aat gct aaa gaa cca aca ttc ttg tat gca atg cca ttt gat Val Asn Asn Ala Lys Glu Pro Thr Phe Leu Tyr Ala Met Pro Phe Asp 275 280 285 290			864

275	280	285	
aga gat ttg gtt ttc ttg gaa gag act tct ttg gtg agt cgt cct gtt Arg Asp Leu Val Phe Leu Glu Glu Thr Ser Leu Val Ser Arg Pro Val 290 295 300			912
tta tcg tat atg gaa gta aaa aga agg atg gtg gca aga tta agg cat Leu Ser Tyr Met Glu Val Lys Arg Arg Met Val Ala Arg Leu Arg His 305 310 315 320			960
ttg ggg atc aaa gtg aaa agt gtt att gag gaa gag aaa tgt gtg atc Leu Gly Ile Lys Val Lys Ser Val Ile Glu Glu Glu Lys Cys Val Ile 325 330 335			1008
cct atg gga gga cca ctt ccg cgg att cct caa aat gtt atg gct att Pro Met Gly Gly Pro Leu Pro Arg Ile Pro Gln Asn Val Met Ala Ile 340 345 350			1056
ggg ggg aat tca ggg ata gtt cat cca tca aca ggg tac atg gtg gct Gly Gly Asn Ser Gly Ile Val His Pro Ser Thr Gly Tyr Met Val Ala 355 360 365			1104
agg agc atg gct tta gca cca gta cta gct gaa gcc atc gtc gag ggg Arg Ser Met Ala Leu Ala Pro Val Leu Ala Glu Ala Ile Val Glu Gly 370 375 380			1152
ctt ggc tca aca aga atg ata aga ggg tct caa ctt tac cat aga gtt Leu Gly Ser Thr Arg Met Ile Arg Gly Ser Gln Leu Tyr His Arg Val 385 390 395 400			1200
tgg aat ggt ttg tgg cct ttg gat aga aga tgt gtt aga gaa tgt tat Trp Asn Gly Leu Trp Pro Leu Asp Arg Arg Cys Val Arg Glu Cys Tyr 405 410 415			1248
tca ttt ggg atg gag aca ttg ttg aag cct gat ttg aaa ggg act agg Ser Phe Gly Met Glu Thr Leu Leu Lys Leu Asp Leu Lys Gly Thr Arg 420 425 430			1296
aga ttg ttt gac gct ttc ttt gat ctt gat cct aaa tac tgg caa ggg Arg Leu Phe Asp Ala Phe Phe Asp Leu Asp Pro Lys Tyr Trp Gln Gly 435 440 445			1344
ttc ctt tct tca aga ttg tct gtc aaa gaa ctt ggt tta ctc agc ttg Phe Leu Ser Ser Arg Leu Ser Val Lys Glu Leu Gly Leu Leu Ser Leu 450 455 460			1392
tgt ctt ttc gga cat ggc tca aac atg act agg ttg gat att gtt aca Cys Leu Phe Gly His Gly Ser Asn Met Thr Arg Leu Asp Ile Val Thr 465 470 475 480			1440
aaa tgt cct ctt cct ttg gtt aga ctg att ggc aat cta gca ata gag Lys Cys Pro Leu Pro Leu Val Arg Leu Ile Gly Asn Leu Ala Ile Glu 485 490 495			1488
agc ctt tgaatgtgaa aagtttgaat cattttcttc attttaattt ctttgattat Ser Leu			1544
tttcatatattt tctcaattgc aaaagtgaga taagagctac atactgtcaa caaataaact			1604

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aa 1666

<210> 96
<211> 498
<212> PRT
<213> Lycopersicon esculentum
<400> 96

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Thr Pro His Arg Ser Ile Phe Gln Gln Asn Pro Ser Phe Leu Ser Pro
20 25 30

Thr Thr Lys Lys Lys Ser Arg Lys Cys Leu Leu Arg Asn Lys Ser Ser
35 40 45

Lys Leu Phe Cys Ser Phe Leu Asp Leu Ala Pro Thr Ser Lys Pro Glu
50 55 60

Ser Leu Asp Val Asn Ile Ser Trp Val Asp Pro Asn Ser Asn Arg Ala
65 70 75 80

Gln Phe Asp Val Ile Ile Ile Gly Ala Gly Pro Ala Gly Leu Arg Leu
85 90 95

Ala Glu Gln Val Ser Lys Tyr Gly Ile Lys Val Cys Cys Val Asp Pro
100 105 110

Ser Pro Leu Ser Met Trp Pro Asn Asn Tyr Gly Val Trp Val Asp Glu
115 120 125

Phe Glu Asn Leu Gly Leu Glu Asn Cys Leu Asp His Lys Trp Pro Met
130 135 140

Thr Cys Val His Ile Asn Asp Asn Lys Thr Lys Tyr Leu Gly Arg Pro
145 150 155 160

Tyr Gly Arg Val Ser Arg Lys Lys Leu Lys Leu Lys Leu Leu Asn Ser
165 170 175

Cys Val Glu Asn Arg Val Lys Phe Tyr Lys Ala Lys Val Trp Lys Val

180					185					190					
Glu	His	Glu	Glu	Phe	Glu	Ser	Ser	Ile	Val	Cys	Asp	Asp	Gly	Lys	Lys
	195					200					205				
Ile	Arg	Gly	Ser	Leu	Val	Val	Asp	Ala	Ser	Gly	Phe	Ala	Ser	Asp	Phe
	210					215					220				
Ile	Glu	Tyr	Asp	Arg	Pro	Arg	Asn	His	Gly	Tyr	Gln	Ile	Ala	His	Gly
	225					230					235				240
Val	Leu	Val	Glu	Val	Asp	Asn	His	Pro	Phe	Asp	Leu	Asp	Lys	Met	Val
				245					250					255	
Leu	Met	Asp	Trp	Arg	Asp	Ser	His	Leu	Gly	Asn	Glu	Pro	Tyr	Leu	Arg
			260					265					270		
Val	Asn	Asn	Ala	Lys	Glu	Pro	Thr	Phe	Leu	Tyr	Ala	Met	Pro	Phe	Asp
		275					280					285			
Arg	Asp	Leu	Val	Phe	Leu	Glu	Glu	Thr	Ser	Leu	Val	Ser	Arg	Pro	Val
	290					295					300				
Leu	Ser	Tyr	Met	Glu	Val	Lys	Arg	Arg	Met	Val	Ala	Arg	Leu	Arg	His
	305					310					315				320
Leu	Gly	Ile	Lys	Val	Lys	Ser	Val	Ile	Glu	Glu	Glu	Lys	Cys	Val	Ile
				325					330					335	
Pro	Met	Gly	Gly	Pro	Leu	Pro	Arg	Ile	Pro	Gln	Asn	Val	Met	Ala	Ile
			340					345					350		
Gly	Gly	Asn	Ser	Gly	Ile	Val	His	Pro	Ser	Thr	Gly	Tyr	Met	Val	Ala
		355					360					365			
Arg	Ser	Met	Ala	Leu	Ala	Pro	Val	Leu	Ala	Glu	Ala	Ile	Val	Glu	Gly
	370					375					380				
Leu	Gly	Ser	Thr	Arg	Met	Ile	Arg	Gly	Ser	Gln	Leu	Tyr	His	Arg	Val
	385					390					395				400
Trp	Asn	Gly	Leu	Trp	Pro	Leu	Asp	Arg	Arg	Cys	Val	Arg	Glu	Cys	Tyr
				405					410					415	
Ser	Phe	Gly	Met	Glu	Thr	Leu	Leu	Lys	Leu	Asp	Leu	Lys	Gly	Thr	Arg

420

425

430

Arg Leu Phe Asp Ala Phe Phe Asp Leu Asp Pro Lys Tyr Trp Gln Gly
 435 440 445

Phe Leu Ser Ser Arg Leu Ser Val Lys Glu Leu Gly Leu Leu Ser Leu
 450 455 460

Cys Leu Phe Gly His Gly Ser Asn Met Thr Arg Leu Asp Ile Val Thr
 465 470 475 480

Lys Cys Pro Leu Pro Leu Val Arg Leu Ile Gly Asn Leu Ala Ile Glu
 485 490 495

Ser Leu

<210> 97

<211> 1125

<212> DNA

<213> Lycopersicon esculentum

<220>

<221> CDS

<222> (20)..(946)

<400> 97

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 Thr Ser Arg Thr Phe Tyr Phe Arg His Ser Pro Phe Leu Gly Pro Lys
 15 20 25

cct act tcg aca acc tca cat gtt tct cca atc tct cct ttt tct ctt 148
 Pro Thr Ser Thr Thr Ser His Val Ser Pro Ile Ser Pro Phe Ser Leu
 30 35 40

aat cta ggc cca att ttg agg tct aga aga aaa ccc agt ttc act gtt 196
 Asn Leu Gly Pro Ile Leu Arg Ser Arg Arg Lys Pro Ser Phe Thr Val
 45 50 55

tgc ttt gtt ctc gag gat gag aag ctg aaa cct caa ttt gac gat gag 244
 Cys Phe Val Leu Glu Asp Glu Lys Leu Lys Pro Gln Phe Asp Asp Glu
 60 65 70 75

gct gag gat ttt gaa aag aag att gag gaa cag atc tta gct act cgc 292

Ala	Glu	Asp	Phe	Glu	Lys	Lys	Ile	Glu	Glu	Gln	Ile	Leu	Ala	Thr	Arg		
				80				85					90				
ttg	gcg	gag	aaa	ctg	gct	agg	aag	aaa	tcg	gag	agg	ttt	act	tat	ctt	340	
Leu	Ala	Glu	Lys	Leu	Ala	Arg	Lys	Lys	Ser	Glu	Arg	Phe	Thr	Tyr	Leu		
				95					100					105			
gtg	gct	gct	ata	atg	tct	agt	ttt	ggg	att	act	tct	atg	gct	gtt	atg	388	
Val	Ala	Ala	Ile	Met	Ser	Ser	Phe	Gly	Ile	Thr	Ser	Met	Ala	Val	Met		
				110					115					120			
gct	gtt	tat	tac	aga	ttt	tcg	tgg	caa	atg	gag	gga	gga	gaa	gtt	cct	436	
Ala	Val	Tyr	Tyr	Arg	Phe	Ser	Trp	Gln	Met	Glu	Gly	Gly	Glu	Val	Pro		
				125					130					135			
gta	acc	gaa	atg	ttg	ggg	aca	ttt	gct	ctc	tct	gtt	ggg	gct	gct	gta	484	
Val	Thr	Glu	Met	Leu	Gly	Thr	Phe	Ala	Leu	Ser	Val	Gly	Ala	Ala	Val		
				140					145					150			
gga	atg	gag	ttt	tgg	gcg	aga	tgg	gca	cac	aaa	gca	ctg	tgg	cat	gct	532	
Gly	Met	Glu	Phe	Trp	Ala	Arg	Trp	Ala	His	Lys	Ala	Leu	Trp	His	Ala		
				160					165					170			
tca	cta	tgg	cac	atg	cat	gag	tca	cac	cac	aaa	cca	aga	gaa	gga	cct	580	
Ser	Leu	Trp	His	Met	His	Glu	Ser	His	His	Lys	Pro	Arg	Glu	Gly	Pro		
				175					180					185			
ttt	gag	ctg	aac	gac	gtt	ttc	gcc	ata	aca	aac	gct	gtt	cca	gca	ata	628	
Phe	Glu	Leu	Asn	Asp	Val	Phe	Ala	Ile	Thr	Asn	Ala	Val	Pro	Ala	Ile		
				190					195					200			
gcc	ctc	ctc	aac	tat	ggg	ttc	ttc	cat	aaa	ggc	ctc	att	gcc	gga	cta	676	
Ala	Leu	Leu	Asn	Tyr	Gly	Phe	Phe	His	Lys	Gly	Leu	Ile	Ala	Gly	Leu		
				205					210					215			
tgc	ttc	ggg	gct	ggg	cta	ggg	atc	aca	gta	ttt	gga	atg	gca	tac	atg	724	
Cys	Phe	Gly	Ala	Gly	Leu	Gly	Ile	Thr	Val	Phe	Gly	Met	Ala	Tyr	Met		
				220					225					230			
ttt	gtt	cac	gat	ggg	ttg	gtt	cac	aag	aga	ttc	cca	gtt	gga	cct	gta	772	
Phe	Val	His	Asp	Gly	Leu	Val	His	Lys	Arg	Phe	Pro	Val	Gly	Pro	Val		
				240					245					250			
gcc	aat	gta	cct	tat	ctt	agg	aag	gtg	gct	gct	gct	cat	tcg	ctt	cat	820	
Ala	Asn	Val	Pro	Tyr	Leu	Arg	Lys	Val	Ala	Ala	Ala	His	Ser	Leu	His		
				255					260					265			
cac	tca	gag	aag	ttc	aat	ggg	gtc	cca	tat	ggc	ttg	ttc	ttc	gga	cct	868	
His	Ser	Glu	Lys	Phe	Asn	Gly	Val	Pro	Tyr	Gly	Leu	Phe	Phe	Gly	Pro		
				270					275					280			
aag	gaa	ctg	gaa	gaa	gta	gga	ggg	acg	gaa	gag	ttg	gaa	aag	gaa	gtg	916	
Lys	Glu	Leu	Glu	Glu	Val	Gly	Gly	Thr	Glu	Glu	Leu	Glu	Lys	Glu	Val		
				285					290					295			
ata	cga	agg	acg	aga	ctt	tcg	aaa	gga	tca	tga	acg	attg	ttc	ata	aaca	966	
Ile	Arg	Arg	Thr	Arg	Leu	Ser	Lys	Gly	Ser								
				300					305								
taga																	

tagagaaaaa tgtagctctc ttgatgaaat gaatttgtat ttatgtaggc tcttcttatt 1086
 cagtaagatt ttttcttttt tttgatctcg tgccgaatt 1125

<210> 98

<211> 309

<212> PRT

<213> Lycopersicon esculentum

<400> 98

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Tyr Phe Arg His Ser Pro Phe Leu Gly Pro Lys Pro Thr Ser Thr Thr
 20 25 30

Ser His Val Ser Pro Ile Ser Pro Phe Ser Leu Asn Leu Gly Pro Ile
 35 40 45

Leu Arg Ser Arg Arg Lys Pro Ser Phe Thr Val Cys Phe Val Leu Glu
 50 55 60

Asp Glu Lys Leu Lys Pro Gln Phe Asp Asp Glu Ala Glu Asp Phe Glu
 65 70 75 80

Lys Lys Ile Glu Glu Gln Ile Leu Ala Thr Arg Leu Ala Glu Lys Leu
 85 90 95

Ala Arg Lys Lys Ser Glu Arg Phe Thr Tyr Leu Val Ala Ala Ile Met
 100 105 110

Ser Ser Phe Gly Ile Thr Ser Met Ala Val Met Ala Val Tyr Tyr Arg
 115 120 125

Phe Ser Trp Gln Met Glu Gly Gly Glu Val Pro Val Thr Glu Met Leu
 130 135 140

Gly Thr Phe Ala Leu Ser Val Gly Ala Ala Val Gly Met Glu Phe Trp
 145 150 155 160

Ala Arg Trp Ala His Lys Ala Leu Trp His Ala Ser Leu Trp His Met
 165 170 175

His Glu Ser His His Lys Pro Arg Glu Gly Pro Phe Glu Leu Asn Asp
 180 185 190

Val Phe Ala Ile Thr Asn Ala Val Pro Ala Ile Ala Leu Leu Asn Tyr
 195 200 205

Gly Phe Phe His Lys Gly Leu Ile Ala Gly Leu Cys Phe Gly Ala Gly
 210 215 220

Leu Gly Ile Thr Val Phe Gly Met Ala Tyr Met Phe Val His Asp Gly
 225 230 235 240

Leu Val His Lys Arg Phe Pro Val Gly Pro Val Ala Asn Val Pro Tyr
 245 250 255

Leu Arg Lys Val Ala Ala Ala His Ser Leu His His Ser Glu Lys Phe
 260 265 270

Asn Gly Val Pro Tyr Gly Leu Phe Phe Gly Pro Lys Glu Leu Glu Glu
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Val Gly Gly Thr Glu Glu Leu Glu Lys Glu Val Ile Arg Arg Thr Arg
 290 295 300

Leu Ser Lys Gly Ser
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<211> 1779

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<213> Arabidopsis thaliana

<220>

<221> CDS

<400> 99

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 Met Asp Leu Arg Arg Arg Pro Pro Lys Pro Pro Val Thr Asn Asn Asn
 1 5 10 15

aac tcc aac gga tct ttc cgt tct tat cag cct cgc act tcc gat gac 96
 Asn Ser Asn Gly Ser Phe Arg Ser Tyr Gln Pro Arg Thr Ser Asp Asp
 20 25 30

gat cat cgt cgc cgg gct aca aca att gct cct cca ccg aaa gca tcc 144
 Asp His Arg Arg Arg Ala Thr Thr Ile Ala Pro Pro Pro Lys Ala Ser

35	40	45	
gac gcg ctt cct ctt ccg tta tat ctc aca aac gcc gtt ttc ttc acg Asp Ala Leu Pro Leu Pro Leu Tyr Leu Thr Asn Ala Val Phe Phe Thr 50 55 60			192
ctc ttc ttc tcc gtc gcg tat tac ctc ctc cac cgg tgg cgt gac aag Leu Phe Phe Ser Val Ala Tyr Tyr Leu Leu His Arg Trp Arg Asp Lys 65 70 75 80			240
atc cgt tac aat acg cct ctt cac gtc gtc act atc aca gaa ctc ggc Ile Arg Tyr Asn Thr Pro Leu His Val Val Thr Ile Thr Glu Leu Gly 85 90 95			288
gcc att att gct ctc atc gct tcg ttt atc tat ctc cta ggg ttt ttt Ala Ile Ile Ala Leu Ile Ala Ser Phe Ile Tyr Leu Leu Gly Phe Phe 100 105 110			336
ggg att gac ttt gtt cag tca ttt atc tca cgt gcc tct ggt gat gct Gly Ile Asp Phe Val Gln Ser Phe Ile Ser Arg Ala Ser Gly Asp Ala 115 120 125			384
tgg gat ctc gcc gat acg atc gat gat gat gac cac cgc ctt gtc acg Trp Asp Leu Ala Asp Thr Ile Asp Asp Asp Asp His Arg Leu Val Thr 130 135 140			432
tgc tct cca ccg act ccg atc gtt tcc gtt gct aaa tta cct aat ccg Cys Ser Pro Pro Thr Pro Ile Val Ser Val Ala Lys Leu Pro Asn Pro 145 150 155 160			480
gaa cct att gtt acc gaa tcg ctt cct gag gaa gac gag gag att gtg Glu Pro Ile Val Thr Glu Ser Leu Pro Glu Glu Asp Glu Glu Ile Val 165 170 175			528
aaa tcg gtt atc gac gga gtt att cca tcg tac tcg ctt gaa tct cgt Lys Ser Val Ile Asp Gly Val Ile Pro Ser Tyr Ser Leu Glu Ser Arg 180 185 190			576
ctc ggt gat tgc aaa aga gcg gcg tcg att cgt cgt gag gcg ttg cag Leu Gly Asp Cys Lys Arg Ala Ala Ser Ile Arg Arg Glu Ala Leu Gln 195 200 205			624
aga gtc acc ggg aga tcg att gaa ggg tta ccg ttg gat gga ttt gat Arg Val Thr Gly Arg Ser Ile Glu Gly Leu Pro Leu Asp Gly Phe Asp 210 215 220			672
tat gaa tcg att ttg ggg caa tgc tgt gag atg cct gtt gga tac att Tyr Glu Ser Ile Leu Gly Gln Cys Cys Glu Met Pro Val Gly Tyr Ile 225 230 235 240			720
cag att cct gtt ggg att gct ggt cca ttg ttg ctt gat ggt tat gag Gln Ile Pro Val Gly Ile Ala Gly Pro Leu Leu Leu Asp Gly Tyr Glu 245 250 255			768
tac tct gtt cct atg gct aca acc gaa ggt tgt ttg gtt gct agc act Tyr Ser Val Pro Met Ala Thr Thr Glu Gly Cys Leu Val Ala Ser Thr 260 265 270			816

aac aga ggc tgc aag gct atg ttt atc tct ggt ggc gcc acc agt acc Asn Arg Gly Cys Lys Ala Met Phe Ile Ser Gly Gly Ala Thr Ser Thr 275 280 285	864
gtt ctt aag gac ggt atg acc cga gca cct gtt gtt cgg ttc gct tcg Val Leu Lys Asp Gly Met Thr Arg Ala Pro Val Val Arg Phe Ala Ser 290 295 300	912
gcg aga cga gct tcg gag ctt aag ttt ttc ttg gag aat cca gag aac Ala Arg Arg Ala Ser Glu Leu Lys Phe Phe Leu Glu Asn Pro Glu Asn 305 310 315 320	960
ttt gat act ttg gca gta gtc ttc aac agg tcg agt aga ttt gca aga Phe Asp Thr Leu Ala Val Val Phe Asn Arg Ser Ser Arg Phe Ala Arg 325 330 335	1008
ctg caa agt gtt aaa tgc aca atc gcg ggg aag aat gct tat gta agg Leu Gln Ser Val Lys Cys Thr Ile Ala Gly Lys Asn Ala Tyr Val Arg 340 345 350	1056
ttc tgt tgt agt act ggt gat gct atg ggg atg aat atg gtt tct aaa Phe Cys Cys Ser Thr Gly Asp Ala Met Gly Met Asn Met Val Ser Lys 355 360 365	1104
ggt gtg cag aat gtt ctt gag tat ctt acc gat gat ttc cct gac atg Gly Val Gln Asn Val Leu Glu Tyr Leu Thr Asp Asp Phe Pro Asp Met 370 375 380	1152
gat gtg att gga atc tct ggt aac ttc tgt tcg gac aag aaa cct gct Asp Val Ile Gly Ile Ser Gly Asn Phe Cys Ser Asp Lys Lys Pro Ala 385 390 395 400	1200
gct gtg aac tgg att gag gga cgt ggt aaa tca gtt gtt tgc gag gct Ala Val Asn Trp Ile Glu Gly Arg Gly Lys Ser Val Val Cys Glu Ala 405 410 415	1248
gta atc aga gga gag atc gtg aac aag gtc ttg aaa acg agc gtg gct Val Ile Arg Gly Glu Ile Val Asn Lys Val Leu Lys Thr Ser Val Ala 420 425 430	1296
gct tta gtc gag ctc aac atg ctc aag aac cta gct ggc tct gct gtt Ala Leu Val Glu Leu Asn Met Leu Lys Asn Leu Ala Gly Ser Ala Val 435 440 445	1344
gca ggc tct cta ggt gga ttc aac gct cat gcc agt aac ata gtg tct Ala Gly Ser Leu Gly Gly Phe Asn Ala His Ala Ser Asn Ile Val Ser 450 455 460	1392
gct gta ttc ata gct act ggc caa gat cca gct caa aac gtg gag agt Ala Val Phe Ile Ala Thr Gly Gln Asp Pro Ala Gln Asn Val Glu Ser 465 470 475 480	1440
tct caa tgc atc acc atg atg gaa gct att aat gac ggc aaa gat atc Ser Gln Cys Ile Thr Met Met Glu Ala Ile Asn Asp Gly Lys Asp Ile 485 490 495	1488
cat atc tca gtc act atg cca tct atc gag gtg ggg aca gtg gga gga His Ile Ser Val Thr Met Pro Ser Ile Glu Val Gly Thr Val Gly Gly	1536

500	505	510	
gga aca cag ctt gca tct caa tca gcg tgt tta aac ctg ctc gga gtt			1584
Gly Thr Gln Leu Ala Ser Gln Ser Ala Cys Leu Asn Leu Leu Gly Val			
515	520	525	
aaa gga gca agc aca gag tcg ccg gga atg aac gca agg agg cta gcg			1632
Lys Gly Ala Ser Thr Glu Ser Pro Gly Met Asn Ala Arg Arg Leu Ala			
530	535	540	
acg atc gta gcc gga gca gtt tta gct gga gag tta tct tta atg tca			1680
Thr Ile Val Ala Gly Ala Val Leu Ala Gly Glu Leu Ser Leu Met Ser			
545	550	555	560
gca att gca gct gga cag ctt gtg aga agt cac atg aaa tac aat aga			1728
Ala Ile Ala Ala Gly Gln Leu Val Arg Ser His Met Lys Tyr Asn Arg			
565	570	575	
tcc agc cga gac atc tct gga gca acg aca acg aca aca aca aca aca			1776
Ser Ser Arg Asp Ile Ser Gly Ala Thr Thr Thr Thr Thr Thr Thr			
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tga			1779
<210>	100		
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<212>	PRT		
<213>	Arabidopsis thaliana		
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Asn Ser Asn Gly Ser Phe Arg Ser Tyr Gln Pro Arg Thr Ser Asp Asp			
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Asp His Arg Arg Arg Ala Thr Thr Ile Ala Pro Pro Pro Lys Ala Ser			
35	40	45	
Asp Ala Leu Pro Leu Pro Leu Tyr Leu Thr Asn Ala Val Phe Phe Thr			
50	55	60	
Leu Phe Phe Ser Val Ala Tyr Tyr Leu Leu His Arg Trp Arg Asp Lys			
65	70	75	80
Ile Arg Tyr Asn Thr Pro Leu His Val Val Thr Ile Thr Glu Leu Gly			
85	90	95	

Ala Ile Ile Ala Leu Ile Ala Ser Phe Ile Tyr Leu Leu Gly Phe Phe
 100 105 110

Gly Ile Asp Phe Val Gln Ser Phe Ile Ser Arg Ala Ser Gly Asp Ala
 115 120 125

Trp Asp Leu Ala Asp Thr Ile Asp Asp Asp Asp His Arg Leu Val Thr
 130 135 140

Cys Ser Pro Pro Thr Pro Ile Val Ser Val Ala Lys Leu Pro Asn Pro
 145 150 155 160

Glu Pro Ile Val Thr Glu Ser Leu Pro Glu Glu Asp Glu Glu Ile Val
 165 170 175

Lys Ser Val Ile Asp Gly Val Ile Pro Ser Tyr Ser Leu Glu Ser Arg
 180 185 190

Leu Gly Asp Cys Lys Arg Ala Ala Ser Ile Arg Arg Glu Ala Leu Gln
 195 200 205

Arg Val Thr Gly Arg Ser Ile Glu Gly Leu Pro Leu Asp Gly Phe Asp
 210 215 220

Tyr Glu Ser Ile Leu Gly Gln Cys Cys Glu Met Pro Val Gly Tyr Ile
 225 230 235 240

Gln Ile Pro Val Gly Ile Ala Gly Pro Leu Leu Leu Asp Gly Tyr Glu
 245 250 255

Tyr Ser Val Pro Met Ala Thr Thr Glu Gly Cys Leu Val Ala Ser Thr
 260 265 270

Asn Arg Gly Cys Lys Ala Met Phe Ile Ser Gly Gly Ala Thr Ser Thr
 275 280 285

Val Leu Lys Asp Gly Met Thr Arg Ala Pro Val Val Arg Phe Ala Ser
 290 295 300

Ala Arg Arg Ala Ser Glu Leu Lys Phe Phe Leu Glu Asn Pro Glu Asn
 305 310 315 320

Phe Asp Thr Leu Ala Val Val Phe Asn Arg Ser Ser Arg Phe Ala Arg
 325 330 335

Leu Gln Ser Val Lys Cys Thr Ile Ala Gly Lys Asn Ala Tyr Val Arg
 340 345 350

Phe Cys Cys Ser Thr Gly Asp Ala Met Gly Met Asn Met Val Ser Lys
 355 360 365

Gly Val Gln Asn Val Leu Glu Tyr Leu Thr Asp Asp Phe Pro Asp Met
 370 375 380

Asp Val Ile Gly Ile Ser Gly Asn Phe Cys Ser Asp Lys Lys Pro Ala
 385 390 395 400

Ala Val Asn Trp Ile Glu Gly Arg Gly Lys Ser Val Val Cys Glu Ala
 405 410 415

Val Ile Arg Gly Glu Ile Val Asn Lys Val Leu Lys Thr Ser Val Ala
 420 425 430

Ala Leu Val Glu Leu Asn Met Leu Lys Asn Leu Ala Gly Ser Ala Val
 435 440 445

Ala Gly Ser Leu Gly Gly Phe Asn Ala His Ala Ser Asn Ile Val Ser
 450 455 460

Ala Val Phe Ile Ala Thr Gly Gln Asp Pro Ala Gln Asn Val Glu Ser
 465 470 475 480

Ser Gln Cys Ile Thr Met Met Glu Ala Ile Asn Asp Gly Lys Asp Ile
 485 490 495

His Ile Ser Val Thr Met Pro Ser Ile Glu Val Gly Thr Val Gly Gly
 500 505 510

Gly Thr Gln Leu Ala Ser Gln Ser Ala Cys Leu Asn Leu Leu Gly Val
 515 520 525

Lys Gly Ala Ser Thr Glu Ser Pro Gly Met Asn Ala Arg Arg Leu Ala
 530 535 540

Thr Ile Val Ala Gly Ala Val Leu Ala Gly Glu Leu Ser Leu Met Ser
 545 550 555 560

Ala Ile Ala Ala Gly Gln Leu Val Arg Ser His Met Lys Tyr Asn Arg
 565 570 575

Ser Ser Arg Asp Ile Ser Gly Ala Thr Thr Thr Thr Thr Thr Thr Thr Thr
580 585 590

<210> 101

<211> 1401

<212> DNA

<213> Arabidopsis thaliana ISPH

<220>

<221> CDS

<400> 101

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ttc gtg cgg gag aat cat ctc tct gga tcc gga tct ctc cgc cgc cgg	96
Phe Val Arg Glu Asn His Leu Ser Gly Ser Gly Ser Leu Arg Arg Arg	
20 25 30	
aaa gct tta tca gtc cgg tgc tcg tct ggc gat gag aac gct cct tcg	144
Lys Ala Leu Ser Val Arg Cys Ser Ser Gly Asp Glu Asn Ala Pro Ser	
35 40 45	
cca tcg gtg gtg atg gac tcc gat ttc gac gcc aag gtg ttc cgt aag	192
Pro Ser Val Val Met Asp Ser Asp Phe Asp Ala Lys Val Phe Arg Lys	
50 55 60	
aac ttg acg aga agc gat aat tac aat cgt aaa ggg ttc ggt cat aag	240
Asn Leu Thr Arg Ser Asp Asn Tyr Asn Arg Lys Gly Phe Gly His Lys	
65 70 75 80	
gag gag aca ctc aag ctc atg aat cga gag tac acc agt gat ata ttg	288
Glu Glu Thr Leu Lys Leu Met Asn Arg Glu Tyr Thr Ser Asp Ile Leu	
85 90 95	
gag aca ctg aaa aca aat ggg tat act tat tct tgg gga gat gtt act	336
Glu Thr Leu Lys Thr Asn Gly Tyr Thr Tyr Ser Trp Gly Asp Val Thr	
100 105 110	
gtg aaa ctc gct aaa gca tat ggt ttt tgc tgg ggt gtt gag cgt gct	384
Val Lys Leu Ala Lys Ala Tyr Gly Phe Cys Trp Gly Val Glu Arg Ala	
115 120 125	
gtt cag att gca tat gaa gca cga aag cag ttt cca gag gag agg ctt	432
Val Gln Ile Ala Tyr Glu Ala Arg Lys Gln Phe Pro Glu Glu Arg Leu	
130 135 140	
tgg att act aac gaa atc att cat aac ccg acc gtc aat aag agg ttg	480
Trp Ile Thr Asn Glu Ile Ile His Asn Pro Thr Val Asn Lys Arg Leu	
145 150 155 160	
gaa gat atg gat gtt aaa att att ccg gtt gag gat tca aag aaa cag	528
Glu Asp Met Asp Val Lys Ile Ile Pro Val Glu Asp Ser Lys Lys Gln	
165 170 175	

ttt gat gta gta gag aaa gat gat gtg gtt atc ctt cct gcg ttt gga Phe Asp Val Val Glu Lys Asp Asp Val Val Ile Leu Pro Ala Phe Gly 180 185 190	576
gct ggt gtt gac gag atg tat gtt ctt aat gat aaa aag gtg caa att Ala Gly Val Asp Glu Met Tyr Val Leu Asn Asp Lys Lys Val Gln Ile 195 200 205	624
gtt gac acg act tgt cct tgg gtg aca aag gtc tgg aac acg gtt gag Val Asp Thr Thr Cys Pro Trp Val Thr Lys Val Trp Asn Thr Val Glu 210 215 220	672
aag cac aag aag ggg gaa tac aca tca gta atc cat ggt aaa tat aat Lys His Lys Lys Gly Glu Tyr Thr Ser Val Ile His Gly Lys Tyr Asn 225 230 235 240	720
cat gaa gag acg att gca act gcg tct ttt gca gga aag tac atc att His Glu Glu Thr Ile Ala Thr Ala Ser Phe Ala Gly Lys Tyr Ile Ile 245 250 255	768
gta aag aac atg aaa gag gca aat tac gtt tgt gat tac att ctc ggt Val Lys Asn Met Lys Glu Ala Asn Tyr Val Cys Asp Tyr Ile Leu Gly 260 265 270	816
ggc caa tac gat gga tct agc tcc aca aaa gag gag ttc atg gag aaa Gly Gln Tyr Asp Gly Ser Ser Ser Thr Lys Glu Glu Phe Met Glu Lys 275 280 285	864
ttc aaa tac gca att tcg aag ggt ttc gat ccc gac aat gac ctt gtc Phe Lys Tyr Ala Ile Ser Lys Gly Phe Asp Pro Asp Asn Asp Leu Val 290 295 300	912
aaa gtt ggt att gca aac caa aca acg atg cta aag gga gaa aca gag Lys Val Gly Ile Ala Asn Gln Thr Thr Met Leu Lys Gly Glu Thr Glu 305 310 315 320	960
gag ata gga aga tta ctc gag aca aca atg atg cgc aag tat gga gtg Glu Ile Gly Arg Leu Leu Glu Thr Thr Met Met Arg Lys Tyr Gly Val 325 330 335	1008
gaa aat gta agc gga cat ttc atc agc ttc aac aca ata tgc gac gct Glu Asn Val Ser Gly His Phe Ile Ser Phe Asn Thr Ile Cys Asp Ala 340 345 350	1056
act caa gag cga caa gac gca atc tat gag cta gtg gaa gag aag att Thr Gln Glu Arg Gln Asp Ala Ile Tyr Glu Leu Val Glu Glu Lys Ile 355 360 365	1104
gac ctc atg cta gtg gtt ggc gga tgg aat tca agt aac acc tct cac Asp Leu Met Leu Val Val Gly Gly Trp Asn Ser Ser Asn Thr Ser His 370 375 380	1152
ctt cag gaa atc tca gag gca cgg gga atc cca tct tac tgg atc gat Leu Gln Glu Ile Ser Glu Ala Arg Gly Ile Pro Ser Tyr Trp Ile Asp 385 390 395 400	1200
agt gag aaa cgg ata gga cct ggg aat aaa ata gcc tat aag ctc cac Ser Glu Lys Arg Ile Gly Pro Gly Asn Lys Ile Ala Tyr Lys Leu His 405 410 415	1248

tat gga gaa ctg gtc gag aag gaa aac ttt ctc cca aag gga cca ata 1296
 Tyr Gly Glu Leu Val Glu Lys Glu Asn Phe Leu Pro Lys Gly Pro Ile
 420 425 430

aca atc ggt gtg aca tca ggt gca tca acc ccg gat aag gtc gtg gaa 1344
 Thr Ile Gly Val Thr Ser Gly Ala Ser Thr Pro Asp Lys Val Val Glu
 435 440 445

gat gct ttg gtg aag gtg ttc gac att aaa cgt gaa gag tta ttg cag 1392
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ctg gct tga 1401
 Leu Ala
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<210> 102

<211> 466

<212> PRT

<213> Arabidopsis thaliana ISPH

<400> 102

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 20 25 30

Lys Ala Leu Ser Val Arg Cys Ser Ser Gly Asp Glu Asn Ala Pro Ser
 35 40 45

Pro Ser Val Val Met Asp Ser Asp Phe Asp Ala Lys Val Phe Arg Lys
 50 55 60

Asn Leu Thr Arg Ser Asp Asn Tyr Asn Arg Lys Gly Phe Gly His Lys
 65 70 75 80

Glu Glu Thr Leu Lys Leu Met Asn Arg Glu Tyr Thr Ser Asp Ile Leu
 85 90 95

Glu Thr Leu Lys Thr Asn Gly Tyr Thr Tyr Ser Trp Gly Asp Val Thr
 100 105 110

Val Lys Leu Ala Lys Ala Tyr Gly Phe Cys Trp Gly Val Glu Arg Ala
 115 120 125

Val Gln Ile Ala Tyr Glu Ala Arg Lys Gln Phe Pro Glu Glu Arg Leu
 130 135 140

Trp Ile Thr Asn Glu Ile Ile His Asn Pro Thr Val Asn Lys Arg Leu
 145 150 155 160

Glu Asp Met Asp Val Lys Ile Ile Pro Val Glu Asp Ser Lys Lys Gln
 165 170 175

Phe Asp Val Val Glu Lys Asp Asp Val Val Ile Leu Pro Ala Phe Gly
 180 185 190

Ala Gly Val Asp Glu Met Tyr Val Leu Asn Asp Lys Lys Val Gln Ile
 195 200 205

Val Asp Thr Thr Cys Pro Trp Val Thr Lys Val Trp Asn Thr Val Glu
 210 215 220

Lys His Lys Lys Gly Glu Tyr Thr Ser Val Ile His Gly Lys Tyr Asn
 225 230 235 240

His Glu Glu Thr Ile Ala Thr Ala Ser Phe Ala Gly Lys Tyr Ile Ile
 245 250 255

Val Lys Asn Met Lys Glu Ala Asn Tyr Val Cys Asp Tyr Ile Leu Gly
 260 265 270

Gly Gln Tyr Asp Gly Ser Ser Ser Thr Lys Glu Glu Phe Met Glu Lys
 275 280 285

Phe Lys Tyr Ala Ile Ser Lys Gly Phe Asp Pro Asp Asn Asp Leu Val
 290 295 300

Lys Val Gly Ile Ala Asn Gln Thr Thr Met Leu Lys Gly Glu Thr Glu
 305 310 315 320

Glu Ile Gly Arg Leu Leu Glu Thr Thr Met Met Arg Lys Tyr Gly Val
 325 330 335

Glu Asn Val Ser Gly His Phe Ile Ser Phe Asn Thr Ile Cys Asp Ala
 340 345 350

Thr Gln Glu Arg Gln Asp Ala Ile Tyr Glu Leu Val Glu Glu Lys Ile
 355 360 365

Asp Leu Met Leu Val Val Gly Gly Trp Asn Ser Ser Asn Thr Ser His
 370 375 380

Leu Gln Glu Ile Ser Glu Ala Arg Gly Ile Pro Ser Tyr Trp Ile Asp
 385 390 395 400

Ser Glu Lys Arg Ile Gly Pro Gly Asn Lys Ile Ala Tyr Lys Leu His
 405 410 415

Tyr Gly Glu Leu Val Glu Lys Glu Asn Phe Leu Pro Lys Gly Pro Ile
 420 425 430

Thr Ile Gly Val Thr Ser Gly Ala Ser Thr Pro Asp Lys Val Val Glu
 435 440 445

Asp Ala Leu Val Lys Val Phe Asp Ile Lys Arg Glu Glu Leu Leu Gln
 450 455 460

Leu Ala
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<210> 103

<211> 2160

<212> DNA

<213> Lycopersicon esculentum

<220>

<221> CDS

<400> 103

atg gct ttg tgt gct tat gca ttt cct ggg att ttg aac agg act ggt 48
 Met Ala Leu Cys Ala Tyr Ala Phe Pro Gly Ile Leu Asn Arg Thr Gly
 1 5 10 15

gtg gtt tca gat tct tct aag gca acc cct ttg ttc tct gga tgg att 96
 Val Val Ser Asp Ser Ser Lys Ala Thr Pro Leu Phe Ser Gly Trp Ile
 20 25 30

cat gga aca gat ctg cag ttt ttg ttc caa cac aag ctt act cat gag 144
 His Gly Thr Asp Leu Gln Phe Leu Phe Gln His Lys Leu Thr His Glu
 35 40 45

gtc aag aaa agg tca cgt gtg gtt cag gct tcc tta tca gaa tct gga 192
 Val Lys Lys Arg Ser Arg Val Val Gln Ala Ser Leu Ser Glu Ser Gly
 50 55 60

gaa tac tac aca cag aga ccg cca acg cct att ttg gac act gtg aac 240
 Glu Tyr Tyr Thr Gln Arg Pro Pro Thr Pro Ile Leu Asp Thr Val Asn

65	70	75	80	
tat ccc att cat atg aaa aat ctg tct ctg aag gaa ctt aaa caa cta				288
Tyr Pro Ile His Met Lys Asn Leu Ser Leu Lys Glu Leu Lys Gln Leu	85	90	95	
gca gat gaa cta agg tca gat aca att ttc aat gta tca aag act ggg				336
Ala Asp Glu Leu Arg Ser Asp Thr Ile Phe Asn Val Ser Lys Thr Gly	100	105	110	
ggt cac ctt ggc tca agt ctt ggt gtt gtt gag ctg act gtt gct ctt				384
Gly His Leu Gly Ser Ser Leu Gly Val Val Glu Leu Thr Val Ala Leu	115	120	125	
cat tat gtc ttc aat gca ccg caa gat agg att ctc tgg gat gtt ggt				432
His Tyr Val Phe Asn Ala Pro Gln Asp Arg Ile Leu Trp Asp Val Gly	130	135	140	
cat cag tct tat cct cac aaa atc ttg act ggt aga agg gac aag atg				480
His Gln Ser Tyr Pro His Lys Ile Leu Thr Gly Arg Arg Asp Lys Met	145	150	155	160
tcg aca tta agg cag aca gat ggt ctt gca gga ttt act aag cga tcg				528
Ser Thr Leu Arg Gln Thr Asp Gly Leu Ala Gly Phe Thr Lys Arg Ser	165	170	175	
gag agt gaa tat gat tgc ttt ggc acc ggc cac agt tcc acc acc atc				576
Glu Ser Glu Tyr Asp Cys Phe Gly Thr Gly His Ser Ser Thr Thr Ile	180	185	190	
tca gca ggc cta ggg atg gct gtt ggt aga gat cta aaa gga aga aac				624
Ser Ala Gly Leu Gly Met Ala Val Gly Arg Asp Leu Lys Gly Arg Asn	195	200	205	
aac aat gtt att gcc gta ata ggt gat ggt gcc atg aca gca ggt caa				672
Asn Asn Val Ile Ala Val Ile Gly Asp Gly Ala Met Thr Ala Gly Gln	210	215	220	
gct tat gaa gcc atg aat aat gct ggt tac ctg gac tct gac atg att				720
Ala Tyr Glu Ala Met Asn Asn Ala Gly Tyr Leu Asp Ser Asp Met Ile	225	230	235	240
ggt atc tta aac gac aat aga caa gtt tct tta cct act gct act ctg				768
Val Ile Leu Asn Asp Asn Arg Gln Val Ser Leu Pro Thr Ala Thr Leu	245	250	255	
gat ggg cca gtt gct cct gtt gga gct cta agt agt gct ttg agc agg				816
Asp Gly Pro Val Ala Pro Val Gly Ala Leu Ser Ser Ala Leu Ser Arg	260	265	270	
tta cag tct aat agg cct ctc aga gaa cta aga gaa gtc gca aag gga				864
Leu Gln Ser Asn Arg Pro Leu Arg Glu Leu Arg Glu Val Ala Lys Gly	275	280	285	
ggt act aag cag att ggt ggt cct atg cat gag ctt gct gca aaa gtt				912
Val Thr Lys Gln Ile Gly Gly Pro Met His Glu Leu Ala Ala Lys Val	290	295	300	
gat gaa tat gct cgt ggc atg att agt ggt tct gga tca aca ttg ttt				960
Asp Glu Tyr Ala Arg Gly Met Ile Ser Gly Ser Gly Ser Thr Leu Phe				

305	310	315	320	
gaa gaa ctt gga ctt tac tat att ggt cct gtg gat ggt cac aac att Glu Glu Leu Gly Leu Tyr Tyr Ile Gly Pro Val Asp Gly His Asn Ile	325	330	335	1008
gat gat cta att gcg att ctc aaa gag gtt aga agt act aaa aca aca Asp Asp Leu Ile Ala Ile Leu Lys Glu Val Arg Ser Thr Lys Thr Thr	340	345	350	1056
ggg cca gta ctg atc cat gtt gtc act gag aaa ggc aga ggt tat cca Gly Pro Val Leu Ile His Val Val Thr Glu Lys Gly Arg Gly Tyr Pro	355	360	365	1104
tat gct gag aga gct gca gat aag tat cat gga gtt gcc aag ttt gat Tyr Ala Glu Arg Ala Ala Asp Lys Tyr His Gly Val Ala Lys Phe Asp	370	375	380	1152
cca gca aca gga aag caa ttc aaa gcc agt gcc aag aca cag tcc tat Pro Ala Thr Gly Lys Gln Phe Lys Ala Ser Ala Lys Thr Gln Ser Tyr	385	390	395	1200
aca aca tat ttt gcc gag gct tta att gca gaa gca gaa gca gat aaa Thr Thr Tyr Phe Ala Glu Ala Leu Ile Ala Glu Ala Glu Ala Asp Lys	405	410	415	1248
gac att gtt gca atc cat gct gcc atg ggg ggt ggg acc gga atg aac Asp Ile Val Ala Ile His Ala Ala Met Gly Gly Gly Thr Gly Met Asn	420	425	430	1296
ctt ttc cat cgt cgc ttc cca aca agg tgt ttt gat gtt gga ata gca Leu Phe His Arg Arg Phe Pro Thr Arg Cys Phe Asp Val Gly Ile Ala	435	440	445	1344
gaa caa cat gca gta acc ttt gct gct gga ttg gct tgt gaa ggc att Glu Gln His Ala Val Thr Phe Ala Ala Gly Leu Ala Cys Glu Gly Ile	450	455	460	1392
aaa cct ttc tgt gca atc tat tcg tct ttc atg cag agg gct tat gac Lys Pro Phe Cys Ala Ile Tyr Ser Ser Phe Met Gln Arg Ala Tyr Asp	465	470	475	1440
cag gta gtg cat gac gtt gat ttg caa aag ctg ccc gtg agg ttt gca Gln Val Val His Asp Val Asp Leu Gln Lys Leu Pro Val Arg Phe Ala	485	490	495	1488
atg gac aga gca ggt ctt gtt gga gca gat ggt cca aca cat tgt ggt Met Asp Arg Ala Gly Leu Val Gly Ala Asp Gly Pro Thr His Cys Gly	500	505	510	1536
gca ttt gat gtt act tac atg gca tgt ctt cct aac atg gtt gta atg Ala Phe Asp Val Thr Tyr Met Ala Cys Leu Pro Asn Met Val Val Met	515	520	525	1584
gct cct tct gat gaa gcg gag cta ttt cac atg gta gca act gct gcc Ala Pro Ser Asp Glu Ala Glu Leu Phe His Met Val Ala Thr Ala Ala	530	535	540	1632
gcc att gat gac aga cca agt tgt ttt aga tac cca aga gga aat ggg Ala Ile Asp Asp Arg Pro Ser Cys Phe Arg Tyr Pro Arg Gly Asn Gly				1680

545	550	555	560	
atc ggt gta gag ctt ccg gct gga aac aaa gga att cct ctt gag gtt				1728
Ile Gly Val Glu Leu Pro Ala Gly Asn Lys Gly Ile Pro Leu Glu Val	565	570	575	
ggt aaa ggt agg ata ttg att gag ggg gag aga gtg gct cta ttg gga				1776
Gly Lys Gly Arg Ile Leu Ile Glu Gly Glu Arg Val Ala Leu Leu Gly	580	585	590	
tat ggc tca gca gtg cag aac tgt ttg gat gct gct att gtg cta gaa				1824
Tyr Gly Ser Ala Val Gln Asn Cys Leu Asp Ala Ala Ile Val Leu Glu	595	600	605	
tcc cgc ggc tta caa gta aca gtt gca gat gca cgt ttc tgc aaa cca				1872
Ser Arg Gly Leu Gln Val Thr Val Ala Asp Ala Arg Phe Cys Lys Pro	610	615	620	
ctg gac cat gcc ctc ata agg agc ctt gca aaa tca cat gaa gtg cta				1920
Leu Asp His Ala Leu Ile Arg Ser Leu Ala Lys Ser His Glu Val Leu	625	630	635	640
atc act gtc gaa gaa gga tca att gga ggt ttt gga tct cat gtt gtt				1968
Ile Thr Val Glu Glu Gly Ser Ile Gly Gly Phe Gly Ser His Val Val	645	650	655	
cag ttc atg gcc tta gat ggg ctt ctt gat ggc aag ttg aag tgg aga				2016
Gln Phe Met Ala Leu Asp Gly Leu Leu Asp Gly Lys Leu Lys Trp Arg	660	665	670	
cca ata gtt ctt cct gat cga tac att gac cat gga tct cct gtt gat				2064
Pro Ile Val Leu Pro Asp Arg Tyr Ile Asp His Gly Ser Pro Val Asp	675	680	685	
eag ttg gcg gaa gct ggc cta aca cca tct cac att gca gca aca gta				2112
Gln Leu Ala Glu Ala Gly Leu Thr Pro Ser His Ile Ala Ala Thr Val	690	695	700	
ttt aac ata ctt gga caa acc aga gag gct cta gag gtc atg aca taa				2160
Phe Asn Ile Leu Gly Gln Thr Arg Glu Ala Leu Glu Val Met Thr	705	710	715	

<210> 104

<211> 719

<212> PRT

<213> Lycopersicon esculentum

<400> 104

Met	Ala	Leu	Cys	Ala	Tyr	Ala	Phe	Pro	Gly	Ile	Leu	Asn	Arg	Thr	Gly
1				5					10					15	

Val	Val	Ser	Asp	Ser	Ser	Lys	Ala	Thr	Pro	Leu	Phe	Ser	Gly	Trp	Ile
			20					25					30		

His Gly Thr Asp Leu Gln Phe Leu Phe Gln His Lys Leu Thr His Glu
35 40 45

Val Lys Lys Arg Ser Arg Val Val Gln Ala Ser Leu Ser Glu Ser Gly
50 55 60

Glu Tyr Tyr Thr Gln Arg Pro Pro Thr Pro Ile Leu Asp Thr Val Asn
65 70 75 80

Tyr Pro Ile His Met Lys Asn Leu Ser Leu Lys Glu Leu Lys Gln Leu
85 90 95

Ala Asp Glu Leu Arg Ser Asp Thr Ile Phe Asn Val Ser Lys Thr Gly
100 105 110

Gly His Leu Gly Ser Ser Leu Gly Val Val Glu Leu Thr Val Ala Leu
115 120 125

His Tyr Val Phe Asn Ala Pro Gln Asp Arg Ile Leu Trp Asp Val Gly
130 135 140

His Gln Ser Tyr Pro His Lys Ile Leu Thr Gly Arg Arg Asp Lys Met
145 150 155 160

Ser Thr Leu Arg Gln Thr Asp Gly Leu Ala Gly Phe Thr Lys Arg Ser
165 170 175

Glu Ser Glu Tyr Asp Cys Phe Gly Thr Gly His Ser Ser Thr Thr Ile
180 185 190

Ser Ala Gly Leu Gly Met Ala Val Gly Arg Asp Leu Lys Gly Arg Asn
195 200 205

Asn Asn Val Ile Ala Val Ile Gly Asp Gly Ala Met Thr Ala Gly Gln
210 215 220

Ala Tyr Glu Ala Met Asn Asn Ala Gly Tyr Leu Asp Ser Asp Met Ile
225 230 235 240

Val Ile Leu Asn Asp Asn Arg Gln Val Ser Leu Pro Thr Ala Thr Leu
245 250 255

Asp Gly Pro Val Ala Pro Val Gly Ala Leu Ser Ser Ala Leu Ser Arg
260 265 270

Leu Gln Ser Asn Arg Pro Leu Arg Glu Leu Arg Glu Val Ala Lys Gly
 275 280 285

Val Thr Lys Gln Ile Gly Gly Pro Met His Glu Leu Ala Ala Lys Val
 290 295 300

Asp Glu Tyr Ala Arg Gly Met Ile Ser Gly Ser Gly Ser Thr Leu Phe
 305 310 315 320

Glu Glu Leu Gly Leu Tyr Tyr Ile Gly Pro Val Asp Gly His Asn Ile
 325 330 335

Asp Asp Leu Ile Ala Ile Leu Lys Glu Val Arg Ser Thr Lys Thr Thr
 340 345 350

Gly Pro Val Leu Ile His Val Val Thr Glu Lys Gly Arg Gly Tyr Pro
 355 360 365

Tyr Ala Glu Arg Ala Ala Asp Lys Tyr His Gly Val Ala Lys Phe Asp
 370 375 380

Pro Ala Thr Gly Lys Gln Phe Lys Ala Ser Ala Lys Thr Gln Ser Tyr
 385 390 395 400

Thr Thr Tyr Phe Ala Glu Ala Leu Ile Ala Glu Ala Glu Ala Asp Lys
 405 410 415

Asp Ile Val Ala Ile His Ala Ala Met Gly Gly Gly Thr Gly Met Asn
 420 425 430

Leu Phe His Arg Arg Phe Pro Thr Arg Cys Phe Asp Val Gly Ile Ala
 435 440 445

Glu Gln His Ala Val Thr Phe Ala Ala Gly Leu Ala Cys Glu Gly Ile
 450 455 460

Lys Pro Phe Cys Ala Ile Tyr Ser Ser Phe Met Gln Arg Ala Tyr Asp
 465 470 475 480

Gln Val Val His Asp Val Asp Leu Gln Lys Leu Pro Val Arg Phe Ala
 485 490 495

Met Asp Arg Ala Gly Leu Val Gly Ala Asp Gly Pro Thr His Cys Gly
 500 505 510

Ala Phe Asp Val Thr Tyr Met Ala Cys Leu Pro Asn Met Val Val Met
 515 520 525

Ala Pro Ser Asp Glu Ala Glu Leu Phe His Met Val Ala Thr Ala Ala
 530 535 540

Ala Ile Asp Asp Arg Pro Ser Cys Phe Arg Tyr Pro Arg Gly Asn Gly
 545 550 555 560

Ile Gly Val Glu Leu Pro Ala Gly Asn Lys Gly Ile Pro Leu Glu Val
 565 570 575

Gly Lys Gly Arg Ile Leu Ile Glu Gly Glu Arg Val Ala Leu Leu Gly
 580 585 590

Tyr Gly Ser Ala Val Gln Asn Cys Leu Asp Ala Ala Ile Val Leu Glu
 595 600 605

Ser Arg Gly Leu Gln Val Thr Val Ala Asp Ala Arg Phe Cys Lys Pro
 610 615 620

Leu Asp His Ala Leu Ile Arg Ser Leu Ala Lys Ser His Glu Val Leu
 625 630 635 640

Ile Thr Val Glu Glu Gly Ser Ile Gly Gly Phe Gly Ser His Val Val
 645 650 655

Gln Phe Met Ala Leu Asp Gly Leu Leu Asp Gly Lys Leu Lys Trp Arg
 660 665 670

Pro Ile Val Leu Pro Asp Arg Tyr Ile Asp His Gly Ser Pro Val Asp
 675 680 685

Gln Leu Ala Glu Ala Gly Leu Thr Pro Ser His Ile Ala Ala Thr Val
 690 695 700

Phe Asn Ile Leu Gly Gln Thr Arg Glu Ala Leu Glu Val Met Thr
 705 710 715

<210> 105

<211> 1434

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<400> 105

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Met Met Thr Leu Asn Ser Leu Ser Pro Ala Glu Ser Lys Ala Ile Ser	
1 5 10 15	
ttc ttg gat acc tcc agg ttc aat cca atc cct aaa ctc tca ggt ggg	96
Phe Leu Asp Thr Ser Arg Phe Asn Pro Ile Pro Lys Leu Ser Gly Gly	
20 25 30	
ttt agt ttg agg agg agg aat caa ggg aga ggt ttt gga aaa ggt gtt	144
Phe Ser Leu Arg Arg Arg Asn Gln Gly Arg Gly Phe Gly Lys Gly Val	
35 40 45	
aag tgt tca gtg aaa gtg cag cag caa caa caa cct cct cca gca tgg	192
Lys Cys Ser Val Lys Val Gln Gln Gln Gln Pro Pro Pro Ala Trp	
50 55 60	
cct ggg aga gct gtc cct gag gcg cct cgt caa tct tgg gat gga cca	240
Pro Gly Arg Ala Val Pro Glu Ala Pro Arg Gln Ser Trp Asp Gly Pro	
65 70 75 80	
aaa ccc atc tct atc gtt gga tct act ggt tct att ggc act cag aca	288
Lys Pro Ile Ser Ile Val Gly Ser Thr Gly Ser Ile Gly Thr Gln Thr	
85 90 95	
ttg gat att gtg gct gag aat cct gac aaa ttc aga gtt gtg gct cta	336
Leu Asp Ile Val Ala Glu Asn Pro Asp Lys Phe Arg Val Val Ala Leu	
100 105 110	
gct gct ggt tcg aat gtt act cta ctt gct gat cag gta agg aga ttt	384
Ala Ala Gly Ser Asn Val Thr Leu Leu Ala Asp Gln Val Arg Arg Phe	
115 120 125	
aag cct gca ttg gtt gct gtt aga aac gag tca ctg att aat gag ctt	432
Lys Pro Ala Leu Val Ala Val Arg Asn Glu Ser Leu Ile Asn Glu Leu	
130 135 140	
aaa gag gct tta gct gat ttg gac tat aaa ctc gag att att cca gga	480
Lys Glu Ala Leu Ala Asp Leu Asp Tyr Lys Leu Glu Ile Ile Pro Gly	
145 150 155 160	
gag caa gga gtg att gag gtt gcc cga cat cct gaa gct gta acc gtt	528
Glu Gln Gly Val Ile Glu Val Ala Arg His Pro Glu Ala Val Thr Val	
165 170 175	
gtt acc gga ata gta ggt tgt gcg gga cta aag cct acg gtt gct gca	576
Val Thr Gly Ile Val Gly Cys Ala Gly Leu Lys Pro Thr Val Ala Ala	
180 185 190	
att gaa gca gga aag gac att gct ctt gca aac aaa gag aca tta atc	624
Ile Glu Ala Gly Lys Asp Ile Ala Leu Ala Asn Lys Glu Thr Leu Ile	
195 200 205	
gca ggt ggt cct ttc gtg ctt ccg ctt gcc aac aaa cat aat gta aag	672
Ala Gly Gly Pro Phe Val Leu Pro Leu Ala Asn Lys His Asn Val Lys	

210	215	220	
att ctt ccg gca gat tca gaa cat tct gcc ata ttt cag tgt att caa Ile Leu Pro Ala Asp Ser Glu His Ser Ala Ile Phe Gln Cys Ile Gln 225 230 235 240			720
ggt ttg cct gaa ggc gct ctg cgc aag ata atc ttg act gca tct ggt Gly Leu Pro Glu Gly Ala Leu Arg Lys Ile Ile Leu Thr Ala Ser Gly 245 250 255			768
gga gct ttt agg gat tgg cct gtc gaa aag cta aag gaa gtt aaa gta Gly Ala Phe Arg Asp Trp Pro Val Glu Lys Leu Lys Glu Val Lys Val 260 265 270			816
gcg gat gcg ttg aag cat cca aac tgg aac atg gga aag aaa atc act Ala Asp Ala Leu Lys His Pro Asn Trp Asn Met Gly Lys Lys Ile Thr 275 280 285			864
gtg gac tct gct acg ctt ttc aac aag ggt ctt gag gtc att gaa gcg Val Asp Ser Ala Thr Leu Phe Asn Lys Gly Leu Glu Val Ile Glu Ala 290 295 300			912
cat tat ttg ttt gga gct gag tat gac gat ata gag att gtc att cat His Tyr Leu Phe Gly Ala Glu Tyr Asp Asp Ile Glu Ile Val Ile His 305 310 315 320			960
ccg caa agt atc ata cat tcc atg att gaa aca cag gat tca tct gtg Pro Gln Ser Ile Ile His Ser Met Ile Glu Thr Gln Asp Ser Ser Val 325 330 335			1008
ctt gct caa ttg ggt tgg cct gat atg cgt tta ccg att ctc tac acc Leu Ala Gln Leu Gly Trp Pro Asp Met Arg Leu Pro Ile Leu Tyr Thr 340 345 350			1056
atg tca tgg ccc gat aga gtt cct tgt tct gaa gta act tgg cca aga Met Ser Trp Pro Asp Arg Val Pro Cys Ser Glu Val Thr Trp Pro Arg 355 360 365			1104
ctt gac ctt tgc aaa ctc ggt tca ttg act ttc aag aaa cca gac aat Leu Asp Leu Cys Lys Leu Gly Ser Leu Thr Phe Lys Lys Pro Asp Asn 370 375 380			1152
gtg aaa tac cca tcc atg gat ctt gct tat gct gct gga cga gct gga Val Lys Tyr Pro Ser Met Asp Leu Ala Tyr Ala Ala Gly Arg Ala Gly 385 390 395 400			1200
ggc aca atg act gga gtt ctc agc gcc gcc aat gag aaa gct gtt gaa Gly Thr Met Thr Gly Val Leu Ser Ala Ala Asn Glu Lys Ala Val Glu 405 410 415			1248
atg ttc att gat gaa aag ata agc tat ttg gat atc ttc aag gtt gtg Met Phe Ile Asp Glu Lys Ile Ser Tyr Leu Asp Ile Phe Lys Val Val 420 425 430			1296
gaa tta aca tgc gat aaa cat cga aac gag ttg gta aca tca ccg tct Glu Leu Thr Cys Asp Lys His Arg Asn Glu Leu Val Thr Ser Pro Ser 435 440 445			1344
ctt gaa gag att gtt cac tat gac ttg tgg gca cgt gaa tat gcc gcg Leu Glu Glu Ile Val His Tyr Asp Leu Trp Ala Arg Glu Tyr Ala Ala 450 455 460			1392

450

455

460

aat gtg cag ctt tct tct ggt gct agg cca gtt cat gca tga
 Asn Val Gln Leu Ser Ser Gly Ala Arg Pro Val His Ala
 465 470 475

1434

<210> 106

<211> 477

<212> PRT

<213> Arabidopsis thaliana

<400> 106

Met Met Thr Leu Asn Ser Leu Ser Pro Ala Glu Ser Lys Ala Ile Ser
 1 5 10 15

Phe Leu Asp Thr Ser Arg Phe Asn Pro Ile Pro Lys Leu Ser Gly Gly
 20 25 30

Phe Ser Leu Arg Arg Arg Asn Gln Gly Arg Gly Phe Gly Lys Gly Val
 35 40 45

Lys Cys Ser Val Lys Val Gln Gln Gln Gln Gln Pro Pro Pro Ala Trp
 50 55 60

Pro Gly Arg Ala Val Pro Glu Ala Pro Arg Gln Ser Trp Asp Gly Pro
 65 70 75 80

Lys Pro Ile Ser Ile Val Gly Ser Thr Gly Ser Ile Gly Thr Gln Thr
 85 90 95

Leu Asp Ile Val Ala Glu Asn Pro Asp Lys Phe Arg Val Val Ala Leu
 100 105 110

Ala Ala Gly Ser Asn Val Thr Leu Leu Ala Asp Gln Val Arg Arg Phe
 115 120 125

Lys Pro Ala Leu Val Ala Val Arg Asn Glu Ser Leu Ile Asn Glu Leu
 130 135 140

Lys Glu Ala Leu Ala Asp Leu Asp Tyr Lys Leu Glu Ile Ile Pro Gly
 145 150 155 160

Glu Gln Gly Val Ile Glu Val Ala Arg His Pro Glu Ala Val Thr Val
 165 170 175

Val Thr Gly Ile Val Gly Cys Ala Gly Leu Lys Pro Thr Val Ala Ala
 180 185 190

Ile Glu Ala Gly Lys Asp Ile Ala Leu Ala Asn Lys Glu Thr Leu Ile
 195 200 205

Ala Gly Gly Pro Phe Val Leu Pro Leu Ala Asn Lys His Asn Val Lys
 210 215 220

Ile Leu Pro Ala Asp Ser Glu His Ser Ala Ile Phe Gln Cys Ile Gln
 225 230 235 240

Gly Leu Pro Glu Gly Ala Leu Arg Lys Ile Ile Leu Thr Ala Ser Gly
 245 250 255

Gly Ala Phe Arg Asp Trp Pro Val Glu Lys Leu Lys Glu Val Lys Val
 260 265 270

Ala Asp Ala Leu Lys His Pro Asn Trp Asn Met Gly Lys Lys Ile Thr
 275 280 285

Val Asp Ser Ala Thr Leu Phe Asn Lys Gly Leu Glu Val Ile Glu Ala
 290 295 300

His Tyr Leu Phe Gly Ala Glu Tyr Asp Asp Ile Glu Ile Val Ile His
 305 310 315 320

Pro Gln Ser Ile Ile His Ser Met Ile Glu Thr Gln Asp Ser Ser Val
 325 330 335

Leu Ala Gln Leu Gly Trp Pro Asp Met Arg Leu Pro Ile Leu Tyr Thr
 340 345 350

Met Ser Trp Pro Asp Arg Val Pro Cys Ser Glu Val Thr Trp Pro Arg
 355 360 365

Leu Asp Leu Cys Lys Leu Gly Ser Leu Thr Phe Lys Lys Pro Asp Asn
 370 375 380

Val Lys Tyr Pro Ser Met Asp Leu Ala Tyr Ala Ala Gly Arg Ala Gly
 385 390 395 400

Gly Thr Met Thr Gly Val Leu Ser Ala Ala Asn Glu Lys Ala Val Glu
 405 410 415

Met Phe Ile Asp Glu Lys Ile Ser Tyr Leu Asp Ile Phe Lys Val Val
 420 425 430

Glu Leu Thr Cys Asp Lys His Arg Asn Glu Leu Val Thr Ser Pro Ser
 435 440 445

Leu Glu Glu Ile Val His Tyr Asp Leu Trp Ala Arg Glu Tyr Ala Ala
 450 455 460

Asn Val Gln Leu Ser Ser Gly Ala Arg Pro Val His Ala
 465 470 475

<210> 107

<211> 884

<212> DNA

<213> Adonis palaestina clone ApIPI28

<220>

<221> CDS

<222> (180)..(884)

<400> 107

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cttcgtgttc ttctcccgt gttcatcttc agcagcggtg tcgtactctt tctatttctt 120

cttccatcac taacagtcct cgccgagggt tgaatcggct gttcgccctca acgtcgact 179

atg ggt gaa gtc gct gat gct ggt atg gat gcc gtc cag aag cgg ctt 227

Met Gly Glu Val Ala Asp Ala Gly Met Asp Ala Val Gln Lys Arg Leu
 1 5 10 15

atg ttc gac gat gaa tgt att ttg gtg gat gag aat gac aag gtc gtc 275

Met Phe Asp Asp Glu Cys Ile Leu Val Asp Glu Asn Asp Lys Val Val
 20 25 30

gga cat gat tcc aaa tac aac tgt cat ttg atg gaa aag ata gag gca 323

Gly His Asp Ser Lys Tyr Asn Cys His Leu Met Glu Lys Ile Glu Ala
 35 40 45

gaa aac ttg ctt cac aga gcc ttc agt gtt ttc tta ttc aac tca aaa 371

Glu Asn Leu Leu His Arg Ala Phe Ser Val Phe Leu Phe Asn Ser Lys
 50 55 60

tac gag ttg ctt ctt cag caa cga tct gca acg aag gta aca ttc ccg 419

Tyr Glu Leu Leu Leu Gln Gln Arg Ser Ala Thr Lys Val Thr Phe Pro
 65 70 75 80

ctc gta tgg aca aac acc tgt tgc agc cat ccc ctc ttc cgt gat tcc 467

Leu Val Trp Thr Asn Thr Cys Cys Ser His Pro Leu Phe Arg Asp Ser
 85 90 95
 gaa ctc ata gaa gaa aat ttt ctc ggg gta cga aac gct gca caa agg 515
 Glu Leu Ile Glu Glu Asn Phe Leu Gly Val Arg Asn Ala Ala Gln Arg
 100 105 110
 aag ctt tta gac gag cta ggc att cca gct gaa gac gta cca gtt gat 563
 Lys Leu Leu Asp Glu Leu Gly Ile Pro Ala Glu Asp Val Pro Val Asp
 115 120 125
 gaa ttc act cct ctt ggt cgc att ctt tac aaa gct cca tct gac gga 611
 Glu Phe Thr Pro Leu Gly Arg Ile Leu Tyr Lys Ala Pro Ser Asp Gly
 130 135 140
 aaa tgg gga gag cac gaa ctg gac tat ctt ctg ttt att gtc cga gat 659
 Lys Trp Gly Glu His Glu Leu Asp Tyr Leu Leu Phe Ile Val Arg Asp
 145 150 155 160
 gtg aaa tac gat cca aac cca gat gaa gtt gct gac gct aag tac gtt 707
 Val Lys Tyr Asp Pro Asn Pro Asp Glu Val Ala Asp Ala Lys Tyr Val
 165 170 175
 aat cgc gag gag ttg aaa gag ata ctg aga aaa gct gat gca ggt gaa 755
 Asn Arg Glu Glu Leu Lys Glu Ile Leu Arg Lys Ala Asp Ala Gly Glu
 180 185 190
 gag gga ata aag ttg tct cct tgg ttt aga ttg gtt gtg gat aac ttt 803
 Glu Gly Ile Lys Leu Ser Pro Trp Phe Arg Leu Val Val Asp Asn Phe
 195 200 205
 ttg ttc aag tgg tgg gat cat gta gag gag ggg aag att aag gac gtc 851
 Leu Phe Lys Trp Trp Asp His Val Glu Glu Gly Lys Ile Lys Asp Val
 210 215 220
 gcc gac atg aaa act atc cac aag ttg act taa 884
 Ala Asp Met Lys Thr Ile His Lys Leu Thr
 225 230

<210> 108

<211> 234

<212> PRT

<213> Adonis palaestina clone ApIPI28

<400> 108

Met Gly Glu Val Ala Asp Ala Gly Met Asp Ala Val Gln Lys Arg Leu
 1 5 10 15

Met Phe Asp Asp Glu Cys Ile Leu Val Asp Glu Asn Asp Lys Val Val
 20 25 30

Gly His Asp Ser Lys Tyr Asn Cys His Leu Met Glu Lys Ile Glu Ala
 35 40 45

Glu Asn Leu Leu His Arg Ala Phe Ser Val Phe Leu Phe Asn Ser Lys
 50 55 60

Tyr Glu Leu Leu Leu Gln Gln Arg Ser Ala Thr Lys Val Thr Phe Pro
 65 70 75 80

Leu Val Trp Thr Asn Thr Cys Cys Ser His Pro Leu Phe Arg Asp Ser
 85 90 95

Glu Leu Ile Glu Glu Asn Phe Leu Gly Val Arg Asn Ala Ala Gln Arg
 100 105 110

Lys Leu Leu Asp Glu Leu Gly Ile Pro Ala Glu Asp Val Pro Val Asp
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Glu Phe Thr Pro Leu Gly Arg Ile Leu Tyr Lys Ala Pro Ser Asp Gly
 130 135 140

Lys Trp Gly Glu His Glu Leu Asp Tyr Leu Leu Phe Ile Val Arg Asp
 145 150 155 160

Val Lys Tyr Asp Pro Asn Pro Asp Glu Val Ala Asp Ala Lys Tyr Val
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Asn Arg Glu Glu Leu Lys Glu Ile Leu Arg Lys Ala Asp Ala Gly Glu
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Glu Gly Ile Lys Leu Ser Pro Trp Phe Arg Leu Val Val Asp Asn Phe
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Phe Thr Arg Ser Val Ala Arg Ile Ser Ser Lys Phe Leu Arg Asn Arg
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agc ttc tat ggc tcc tct caa tct ctc gcc tct cat cgg ttc gca atc      153
Ser Phe Tyr Gly Ser Ser Gln Ser Leu Ala Ser His Arg Phe Ala Ile
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att ccc gat cag ggt cac tct tgt tct gac tct cca cac aag ggt tac      201
Ile Pro Asp Gln Gly His Ser Cys Ser Asp Ser Pro His Lys Gly Tyr
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gtt tgc aga aca act tat tca ttg aaa tct ccg gtt ttt ggt gga ttt      249
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Ser His Gln Leu Tyr His Gln Ser Ser Ser Leu Val Glu Glu Glu Leu
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gac cca ttt tcg ctt gtt gcc gat gag ctg tca ctt ctt agt aat aag      345
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gag tac ttc ttc aaa agg ggt gtg caa gga aaa cag ttt cgt tca act      441
Glu Tyr Phe Phe Lys Arg Gly Val Gln Gly Lys Gln Phe Arg Ser Thr
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att ttg ctg ctg atg gcg aca gct ctg gat gta cga gtt cca gaa gca      489
Ile Leu Leu Leu Met Ala Thr Ala Leu Asp Val Arg Val Pro Glu Ala
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caa cgg ggt att gct gaa atc act gaa atg ata cac gtc gca agt cta      585
Gln Arg Gly Ile Ala Glu Ile Thr Glu Met Ile His Val Ala Ser Leu
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ctg cac gat gat gtc ttg gat gat gcc gat aca agg cgt ggt gtt ggt      633
Leu His Asp Asp Val Leu Asp Asp Ala Asp Thr Arg Arg Gly Val Gly
      180                               185                               190

tcc tta aat gtt gta atg ggt aac aag atg tcg gta tta gca gga gac      681

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Glu	Val	Val	Ala	Leu	Leu	Ala	Thr	Ala	Val	Glu	His	Leu	Val	Thr	Gly	
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Tyr	Tyr	Met	Gln	Lys	Thr	Tyr	Tyr	Lys	Thr	Ala	Ser	Leu	Ile	Ser	Asn	
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Val	Leu	Ala	Phe	Glu	Tyr	Gly	Arg	Asn	Leu	Gly	Leu	Ala	Phe	Gln	Leu	
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Ile	Asp	Asp	Ile	Leu	Asp	Phe	Thr	Gly	Thr	Ser	Ala	Ser	Leu	Gly	Lys	
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Gly	Ser	Leu	Ser	Asp	Ile	Arg	His	Gly	Val	Ile	Thr	Ala	Pro	Ile	Leu	
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Phe	Ala	Met	Glu	Glu	Phe	Pro	Gln	Leu	Arg	Glu	Val	Val	Asp	Gln	Val	
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gaa	aaa	gat	cct	agg	aat	gtt	gac	att	gct	tta	gag	tat	ctt	ggg	aag	1161
Glu	Lys	Asp	Pro	Arg	Asn	Val	Asp	Ile	Ala	Leu	Glu	Tyr	Leu	Gly	Lys	
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cta	gca	gca	gct	gca	atc	ggg	tct	cta	cct	gaa	aca	gac	aat	gaa	gat	1257
Leu	Ala	Ala	Ala	Ala	Ile	Gly	Ser	Leu	Pro	Glu	Thr	Asp	Asn	Glu	Asp	
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1402

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<213> Arabidopsis thaliana

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 35 40 45

Gly Tyr Val Cys Arg Thr Thr Tyr Ser Leu Lys Ser Pro Val Phe Gly
 50 55 60

Gly Phe Ser His Gln Leu Tyr His Gln Ser Ser Ser Leu Val Glu Glu
 65 70 75 80

Glu Leu Asp Pro Phe Ser Leu Val Ala Asp Glu Leu Ser Leu Leu Ser
 85 90 95

Asn Lys Leu Arg Glu Met Val Leu Ala Glu Val Pro Lys Leu Ala Ser
 100 105 110

Ala Ala Glu Tyr Phe Phe Lys Arg Gly Val Gln Gly Lys Gln Phe Arg
 115 120 125

Ser Thr Ile Leu Leu Leu Met Ala Thr Ala Leu Asp Val Arg Val Pro
 130 135 140

Glu Ala Leu Ile Gly Glu Ser Thr Asp Ile Val Thr Ser Glu Leu Arg
 145 150 155 160

Val Arg Gln Arg Gly Ile Ala Glu Ile Thr Glu Met Ile His Val Ala
 165 170 175

Ser Leu Leu His Asp Asp Val Leu Asp Asp Ala Asp Thr Arg Arg Gly
 180 185 190

Val Gly Ser Leu Asn Val Val Met Gly Asn Lys Met Ser Val Leu Ala
195 200 205

Gly Asp Phe Leu Leu Ser Arg Ala Cys Gly Ala Leu Ala Ala Leu Lys
210 215 220

Asn Thr Glu Val Val Ala Leu Leu Ala Thr Ala Val Glu His Leu Val
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Thr Gly Glu Thr Met Glu Ile Thr Ser Ser Thr Glu Gln Arg Tyr Ser
245 250 255

Met Asp Tyr Tyr Met Gln Lys Thr Tyr Tyr Lys Thr Ala Ser Leu Ile
260 265 270

Ser Asn Ser Cys Lys Ala Val Ala Val Leu Thr Gly Gln Thr Ala Glu
275 280 285

Val Ala Val Leu Ala Phe Glu Tyr Gly Arg Asn Leu Gly Leu Ala Phe
290 295 300

Gln Leu Ile Asp Asp Ile Leu Asp Phe Thr Gly Thr Ser Ala Ser Leu
305 310 315 320

Gly Lys Gly Ser Leu Ser Asp Ile Arg His Gly Val Ile Thr Ala Pro
325 330 335

Ile Leu Phe Ala Met Glu Glu Phe Pro Gln Leu Arg Glu Val Val Asp
340 345 350

Gln Val Glu Lys Asp Pro Arg Asn Val Asp Ile Ala Leu Glu Tyr Leu
355 360 365

Gly Lys Ser Lys Gly Ile Gln Arg Ala Arg Glu Leu Ala Met Glu His
370 375 380

Ala Asn Leu Ala Ala Ala Ala Ile Gly Ser Leu Pro Glu Thr Asp Asn
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Glu Asp Val Lys Arg Ser Arg Arg Ala Leu Ile Asp Leu Thr His Arg
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tat cgt cgt cgt atc caa agc tct tca atg gag acc gat ctc aag tca	144
Tyr Arg Arg Arg Ile Gln Ser Ser Ser Met Glu Thr Asp Leu Lys Ser	
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acc ttt ctc aac gtt tat tct gtt ctc aag tct gac ctt ctt cat gac	192
Thr Phe Leu Asn Val Tyr Ser Val Leu Lys Ser Asp Leu Leu His Asp	
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cct tcc ttc gaa ttc acc aat gaa tct cgt ctc tgg gtt gat cgg atg	240
Pro Ser Phe Glu Phe Thr Asn Glu Ser Arg Leu Trp Val Asp Arg Met	
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Leu Asp Tyr Asn Val Arg Gly Gly Lys Leu Asn Arg Gly Leu Ser Val	
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Val Asp Ser Phe Lys Leu Leu Lys Gln Gly Asn Asp Leu Thr Glu Gln	
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Glu Val Phe Leu Ser Cys Ala Leu Gly Trp Cys Ile Glu Trp Leu Gln	
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gct tat ttc ctt gtg ctt gat gat att atg gat aac tct gtc act cgc	432
Ala Tyr Phe Leu Val Leu Asp Asp Ile Met Asp Asn Ser Val Thr Arg	
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cgt ggt caa cct tgc tgg ttc aga gtt cct cag gtt ggt atg gtt gcc	480
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Ile Asn Asp Gly Ile Leu Leu Arg Asn His Ile His Arg Ile Leu Lys	
165 170 175	
aag cat ttc cgt gat aag cct tac tat gtt gac ctt gtt gat ttg ttt	576

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Asn	Glu	Val	Glu	Leu	Gln	Thr	Ala	Cys	Gly	Gln	Met	Ile	Asp	Leu	Ile		
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Thr	Thr	Phe	Glu	Gly	Glu	Lys	Asp	Leu	Ala	Lys	Tyr	Ser	Leu	Ser	Ile		
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Pro	Val	Ala	Cys	Ala	Leu	Leu	Met	Ala	Gly	Glu	Asn	Leu	Glu	Asn	His		
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Gln	Asp	Asp	Tyr	Leu	Asp	Cys	Phe	Ala	Asp	Pro	Glu	Thr	Leu	Gly	Lys		
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Ile	Gly	Thr	Asp	Ile	Glu	Asp	Phe	Lys	Cys	Ser	Trp	Leu	Val	Val	Lys		
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Tyr	Gly	Lys	Pro	Asp	Pro	Ser	Asn	Val	Ala	Lys	Val	Lys	Asp	Leu	Tyr		
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Lys	Glu	Leu	Asp	Leu	Glu	Gly	Val	Phe	Met	Glu	Tyr	Glu	Ser	Lys	Ser		
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Tyr	Glu	Lys	Leu	Thr	Gly	Ala	Ile	Glu	Gly	His	Gln	Ser	Lys	Ala	Ile		
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caa	gca	gtg	cta	aaa	tcc	ttc	ttg	gct	aag	atc	tac	aag	agg	cag	aag	1152	
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 35 40 45

Thr Phe Leu Asn Val Tyr Ser Val Leu Lys Ser Asp Leu Leu His Asp
 50 55 60

Pro Ser Phe Glu Phe Thr Asn Glu Ser Arg Leu Trp Val Asp Arg Met
 65 70 75 80

Leu Asp Tyr Asn Val Arg Gly Gly Lys Leu Asn Arg Gly Leu Ser Val
 85 90 95

Val Asp Ser Phe Lys Leu Leu Lys Gln Gly Asn Asp Leu Thr Glu Gln
 100 105 110

Glu Val Phe Leu Ser Cys Ala Leu Gly Trp Cys Ile Glu Trp Leu Gln
 115 120 125

Ala Tyr Phe Leu Val Leu Asp Asp Ile Met Asp Asn Ser Val Thr Arg
 130 135 140

Arg Gly Gln Pro Cys Trp Phe Arg Val Pro Gln Val Gly Met Val Ala
 145 150 155 160

Ile Asn Asp Gly Ile Leu Leu Arg Asn His Ile His Arg Ile Leu Lys
 165 170 175

Lys His Phe Arg Asp Lys Pro Tyr Tyr Val Asp Leu Val Asp Leu Phe
 180 185 190

Asn Glu Val Glu Leu Gln Thr Ala Cys Gly Gln Met Ile Asp Leu Ile
 195 200 205

Thr Thr Phe Glu Gly Glu Lys Asp Leu Ala Lys Tyr Ser Leu Ser Ile
 210 215 220

His Arg Arg Ile Val Gln Tyr Lys Thr Ala Tyr Tyr Ser Phe Tyr Leu
 225 230 235 240

Pro Val Ala Cys Ala Leu Leu Met Ala Gly Glu Asn Leu Glu Asn His
 245 250 255

Ile Asp Val Lys Asn Val Leu Val Asp Met Gly Ile Tyr Phe Gln Val
 260 265 270

Gln Asp Asp Tyr Leu Asp Cys Phe Ala Asp Pro Glu Thr Leu Gly Lys
 275 280 285

Ile Gly Thr Asp Ile Glu Asp Phe Lys Cys Ser Trp Leu Val Val Lys
 290 295 300

Ala Leu Glu Arg Cys Ser Glu Glu Gln Thr Lys Ile Leu Tyr Glu Asn
 305 310 315 320

Tyr Gly Lys Pro Asp Pro Ser Asn Val Ala Lys Val Lys Asp Leu Tyr
 325 330 335

Lys Glu Leu Asp Leu Glu Gly Val Phe Met Glu Tyr Glu Ser Lys Ser
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 His Pro Ser Thr Ile Leu Thr Gln Ser Arg Ser Arg Ser Pro Pro Ser
 20 25 30

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 325 330 335
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 Thr Glu Ala Arg Asp Gln Leu Leu Gly Phe Asp Ser Asp Lys Val Ala
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<211> 366

<212> PRT

<213> Sinapis alba

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Leu Ile Thr Leu Lys Pro Ile Ser Leu Thr Pro Lys Arg Thr Val Ser
35 40 45

Ser Ser Ser Ser Ser Ser Leu Ile Thr Lys Glu Asp Asn Asn Leu Lys
50 55 60

Ser Ser Ser Ser Ser Phe Asp Phe Met Ser Tyr Ile Ile Arg Lys Ala
65 70 75 80

Asp Ser Val Asn Lys Ala Leu Asp Ser Ala Val Pro Leu Arg Glu Pro
85 90 95

Leu Lys Ile His Glu Ala Met Arg Tyr Ser Leu Leu Ala Gly Gly Lys
 100 105 110

Arg Val Arg Pro Val Leu Cys Ile Ala Ala Cys Glu Leu Val Gly Gly
 115 120 125

Glu Glu Ser Leu Ala Met Pro Ala Arg Cys Ala Val Glu Met Ile His
 130 135 140

Thr Met Ser Leu Ile His Asp Asp Leu Pro Cys Met Asp Asn Asp Asp
 145 150 155 160

Leu Arg Arg Gly Lys Pro Thr Asn His Lys Val Tyr Gly Glu Asp Val
 165 170 175

Ala Val Leu Ala Gly Asp Ala Leu Leu Ser Phe Ala Phe Glu His Leu
 180 185 190

Ala Ser Ala Thr Ser Ser Glu Val Ser Pro Ala Arg Val Val Arg Ala
 195 200 205

Val Gly Glu Leu Ala Lys Ala Ile Gly Thr Glu Gly Leu Val Ala Gly
 210 215 220

Gln Val Val Asp Ile Ser Ser Glu Gly Leu Asp Leu Asn Asn Val Gly
 225 230 235 240

Leu Glu His Leu Lys Phe Ile His Leu His Lys Thr Ala Ala Leu Leu
 245 250 255

Glu Ala Ser Ala Val Leu Gly Gly Ile Ile Gly Gly Gly Ser Asp Glu
 260 265 270

Glu Ile Glu Arg Leu Arg Lys Phe Ala Arg Cys Ile Gly Leu Leu Phe
 275 280 285

Gln Val Val Asp Asp Ile Leu Asp Val Thr Lys Ser Ser Gln Glu Leu
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Gly Lys Thr Ala Gly Lys Asp Leu Ile Ala Asp Lys Leu Thr Tyr Pro
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Lys Leu Met Gly Leu Glu Lys Ser Arg Glu Phe Ala Glu Lys Leu Asn
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<212> DNA

<213> Erwinia uredovora

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<400> 115

atg aat aat ccg tcg tta ctc aat cat gcg gtc gaa acg atg gca gtt 48
 Met Asn Asn Pro Ser Leu Leu Asn His Ala Val Glu Thr Met Ala Val
 1 5 10 15

ggc tcg aaa agt ttt gcg aca gcc tca aag tta ttt gat gca aaa acc 96
 Gly Ser Lys Ser Phe Ala Thr Ala Ser Lys Leu Phe Asp Ala Lys Thr
 20 25 30

cgg cgc agc gta ctg atg ctc tac gcc tgg tgc cgc cat tgt gac gat 144
 Arg Arg Ser Val Leu Met Leu Tyr Ala Trp Cys Arg His Cys Asp Asp
 35 40 45

gtt att gac gat cag acg ctg ggc ttt cag gcc cgg cag cct gcc tta 192
 Val Ile Asp Asp Gln Thr Leu Gly Phe Gln Ala Arg Gln Pro Ala Leu
 50 55 60

caa acg ccc gaa caa cgt ctg atg caa ctt gag atg aaa acg cgc cag 240
 Gln Thr Pro Glu Gln Arg Leu Met Gln Leu Glu Met Lys Thr Arg Gln
 65 70 75 80

gcc tat gca gga tcg cag atg cac gaa ccg gcg ttt gcg gct ttt cag 288
 Ala Tyr Ala Gly Ser Gln Met His Glu Pro Ala Phe Ala Ala Phe Gln
 85 90 95

gaa gtg gct atg gct cat gat atc gcc ccg gct tac gcg ttt gat cat 336
 Glu Val Ala Met Ala His Asp Ile Ala Pro Ala Tyr Ala Phe Asp His
 100 105 110

ctg gaa ggc ttc gcc atg gat gta cgc gaa gcg caa tac agc caa ctg 384
 Leu Glu Gly Phe Ala Met Asp Val Arg Glu Ala Gln Tyr Ser Gln Leu
 115 120 125

gat gat acg ctg cgc tat tgc tat cac gtt gca ggc gtt gtc ggc ttg 432
 Asp Asp Thr Leu Arg Tyr Cys Tyr His Val Ala Gly Val Val Gly Leu
 130 135 140

atg atg gcg caa atc atg ggc gtg cgg gat aac gcc acg ctg gac cgc 480
 Met Met Ala Gln Ile Met Gly Val Arg Asp Asn Ala Thr Leu Asp Arg

145	150	155	160	
gcc tgt gac ctt ggg ctg gca ttt cag ttg acc aat att gct cgc gat				528
Ala Cys Asp Leu Gly Leu Ala Phe Gln Leu Thr Asn Ile Ala Arg Asp				
	165	170	175	
att gtg gac gat gcg cat gcg ggc cgc tgt tat ctg ccg gca agc tgg				576
Ile Val Asp Asp Ala His Ala Gly Arg Cys Tyr Leu Pro Ala Ser Trp				
	180	185	190	
ctg gag cat gaa ggt ctg aac aaa gag aat tat gcg gca cct gaa aac				624
Leu Glu His Glu Gly Leu Asn Lys Glu Asn Tyr Ala Ala Pro Glu Asn				
	195	200	205	
cgt cag gcg ctg agc cgt atc gcc cgt cgt ttg gtg cag gaa gca gaa				672
Arg Gln Ala Leu Ser Arg Ile Ala Arg Arg Leu Val Gln Glu Ala Glu				
	210	215	220	
cct tac tat ttg tct gcc aca gcc ggc ctg gca ggg ttg ccc ctg cgt				720
Pro Tyr Tyr Leu Ser Ala Thr Ala Gly Leu Ala Gly Leu Pro Leu Arg				
	225	230	235	240
tcc gcc tgg gca atc gct acg gcg aag cag gtt tac cgg aaa ata ggt				768
Ser Ala Trp Ala Ile Ala Thr Ala Lys Gln Val Tyr Arg Lys Ile Gly				
	245	250	255	
gtc aaa gtt gaa cag gcc ggt cag caa gcc tgg gat cag cgg cag tca				816
Val Lys Val Glu Gln Ala Gly Gln Gln Ala Trp Asp Gln Arg Gln Ser				
	260	265	270	
acg acc acg ccc gaa aaa tta acg ctg ctg ctg gcc gcc tct ggt cag				864
Thr Thr Thr Pro Glu Lys Leu Thr Leu Leu Leu Ala Ala Ser Gly Gln				
	275	280	285	
gcc ctt act tcc cgg atg cgg gct cat cct ccc cgc cct gcg cat ctc				912
Ala Leu Thr Ser Arg Met Arg Ala His Pro Pro Arg Pro Ala His Leu				
	290	295	300	
tgg cag cgc ccg ctc tag				930
Trp Gln Arg Pro Leu				
305				

<210> 116

<211> 309

<212> PRT

<213> Erwinia uredovora

<400> 116

Met Asn Asn Pro Ser Leu Leu Asn His Ala Val Glu Thr Met Ala Val
1 5 10 15

Gly Ser Lys Ser Phe Ala Thr Ala Ser Lys Leu Phe Asp Ala Lys Thr

20

25

30

Arg Arg Ser Val Leu Met Leu Tyr Ala Trp Cys Arg His Cys Asp Asp
 35 40 45

Val Ile Asp Asp Gln Thr Leu Gly Phe Gln Ala Arg Gln Pro Ala Leu
 50 55 60

Gln Thr Pro Glu Gln Arg Leu Met Gln Leu Glu Met Lys Thr Arg Gln
 65 70 75 80

Ala Tyr Ala Gly Ser Gln Met His Glu Pro Ala Phe Ala Ala Phe Gln
 85 90 95

Glu Val Ala Met Ala His Asp Ile Ala Pro Ala Tyr Ala Phe Asp His
 100 105 110

Leu Glu Gly Phe Ala Met Asp Val Arg Glu Ala Gln Tyr Ser Gln Leu
 115 120 125

Asp Asp Thr Leu Arg Tyr Cys Tyr His Val Ala Gly Val Val Gly Leu
 130 135 140

Met Met Ala Gln Ile Met Gly Val Arg Asp Asn Ala Thr Leu Asp Arg
 145 150 155 160

Ala Cys Asp Leu Gly Leu Ala Phe Gln Leu Thr Asn Ile Ala Arg Asp
 165 170 175

Ile Val Asp Asp Ala His Ala Gly Arg Cys Tyr Leu Pro Ala Ser Trp
 180 185 190

Leu Glu His Glu Gly Leu Asn Lys Glu Asn Tyr Ala Ala Pro Glu Asn
 195 200 205

Arg Gln Ala Leu Ser Arg Ile Ala Arg Arg Leu Val Gln Glu Ala Glu
 210 215 220

Pro Tyr Tyr Leu Ser Ala Thr Ala Gly Leu Ala Gly Leu Pro Leu Arg
 225 230 235 240

Ser Ala Trp Ala Ile Ala Thr Ala Lys Gln Val Tyr Arg Lys Ile Gly
 245 250 255

Val Lys Val Glu Gln Ala Gly Gln Gln Ala Trp Asp Gln Arg Gln Ser

260

265

270

Thr Thr Thr Pro Glu Lys Leu Thr Leu Leu Leu Ala Ala Ser Gly Gln
 275 280 285

Ala Leu Thr Ser Arg Met Arg Ala His Pro Pro Arg Pro Ala His Leu
 290 295 300

Trp Gln Arg Pro Leu
 305

<210> 117

<211> 1479

<212> DNA

<213> Erwinia uredovora

<220>

<221> CDS

<400> 117

atg aaa cca act acg gta att ggt gca ggc ttc ggt ggc ctg gca ctg	48
Met Lys Pro Thr Thr Val Ile Gly Ala Gly Phe Gly Gly Leu Ala Leu	
1 5 10 15	
gca att cgt cta caa gct gcg ggg atc ccc gtc tta ctg ctt gaa caa	96
Ala Ile Arg Leu Gln Ala Ala Gly Ile Pro Val Leu Leu Leu Glu Gln	
20 25 30	
cgt gat aaa ccc ggc ggt cgg gct tat gtc tac gag gat cag ggg ttt	144
Arg Asp Lys Pro Gly Gly Arg Ala Tyr Val Tyr Glu Asp Gln Gly Phe	
35 40 45	
acc ttt gat gca ggc ccg acg gtt atc acc gat ccc agt gcc att gaa	192
Thr Phe Asp Ala Gly Pro Thr Val Ile Thr Asp Pro Ser Ala Ile Glu	
50 55 60	
gaa ctg ttt gca ctg gca gga aaa cag tta aaa gag tat gtc gaa ctg	240
Glu Leu Phe Ala Leu Ala Gly Lys Gln Leu Lys Glu Tyr Val Glu Leu	
65 70 75 80	
ctg ccg gtt acg ccg ttt tac cgc ctg tgt tgg gag tca ggg aag gtc	288
Leu Pro Val Thr Pro Phe Tyr Arg Leu Cys Trp Glu Ser Gly Lys Val	
85 90 95	
ttt aat tac gat aac gat caa acc cgg ctc gaa gcg cag att cag cag	336
Phe Asn Tyr Asp Asn Asp Gln Thr Arg Leu Glu Ala Gln Ile Gln Gln	
100 105 110	
ttt aat ccc cgc gat gtc gaa ggt tat cgt cag ttt ctg gac tat tca	384
Phe Asn Pro Arg Asp Val Glu Gly Tyr Arg Gln Phe Leu Asp Tyr Ser	
115 120 125	

cgc gcg gtg ttt aaa gaa ggc tat cta aag ctc ggt act gtc cct ttt Arg Ala Val Phe Lys Glu Gly Tyr Leu Lys Leu Gly Thr Val Pro Phe 130 135 140	432
tta tcg ttc aga gac atg ctt cgc gcc gca cct caa ctg gcg aaa ctg Leu Ser Phe Arg Asp Met Leu Arg Ala Ala Pro Gln Leu Ala Lys Leu 145 150 155 160	480
cag gca tgg aga agc gtt tac agt aag gtt gcc agt tac atc gaa gat Gln Ala Trp Arg Ser Val Tyr Ser Lys Val Ala Ser Tyr Ile Glu Asp 165 170 175	528
gaa cat ctg cgc cag gcg ttt tct ttc cac tcg ctg ttg gtg ggc ggc Glu His Leu Arg Gln Ala Phe Ser Phe His Ser Leu Leu Val Gly Gly 180 185 190	576
aat ccc ttc gcc acc tca tcc att tat acg ttg ata cac gcg ctg gag Asn Pro Phe Ala Thr Ser Ser Ile Tyr Thr Leu Ile His Ala Leu Glu 195 200 205	624
cgt gag tgg ggc gtc tgg ttt ccg cgt ggc ggc acc ggc gca tta gtt Arg Glu Trp Gly Val Trp Phe Pro Arg Gly Gly Thr Gly Ala Leu Val 210 215 220	672
cag ggg atg ata aag ctg ttt cag gat ctg ggt ggc gaa gtc gtg tta Gln Gly Met Ile Lys Leu Phe Gln Asp Leu Gly Gly Glu Val Val Leu 225 230 235 240	720
aac gcc aga gtc agc cat atg gaa acg aca gga aac aag att gaa gcc Asn Ala Arg Val Ser His Met Glu Thr Thr Gly Asn Lys Ile Glu Ala 245 250 255	768
gtg cat tta gag gac ggt cgc agg ttc ctg acg caa gcc gtc gcg tca Val His Leu Glu Asp Gly Arg Arg Phe Leu Thr Gln Ala Val Ala Ser 260 265 270	816
aat gca gat gtg gtt cat acc tat cgc gac ctg tta agc cag cac cct Asn Ala Asp Val Val His Thr Tyr Arg Asp Leu Leu Ser Gln His Pro 275 280 285	864
gcc gcg gtt aag cag tcc aac aaa ctg cag act aag cgc atg agt aac Ala Ala Val Lys Gln Ser Asn Lys Leu Gln Thr Lys Arg Met Ser Asn 290 295 300	912
tct ctg ttt gtg ctc tat ttt ggt ttg aat cac cat cat gat cag ctc Ser Leu Phe Val Leu Tyr Phe Gly Leu Asn His His His Asp Gln Leu 305 310 315 320	960
gcg cat cac acg gtt tgt ttc ggc ccg cgt tac cgc gag ctg att gac Ala His His Thr Val Cys Phe Gly Pro Arg Tyr Arg Glu Leu Ile Asp 325 330 335	1008
gaa att ttt aat cat gat ggc ctc gca gag gac ttc tca ctt tat ctg Glu Ile Phe Asn His Asp Gly Leu Ala Glu Asp Phe Ser Leu Tyr Leu 340 345 350	1056
cac gcg ccc tgt gtc acg gat tcg tca ctg gcg cct gaa ggt tgc ggc His Ala Pro Cys Val Thr Asp Ser Ser Leu Ala Pro Glu Gly Cys Gly 355 360 365	1104

agt tac tat gtg ttg gcg ccg gtg ccg cat tta ggc acc gcg aac ctc 1152
 Ser Tyr Tyr Val Leu Ala Pro Val Pro His Leu Gly Thr Ala Asn Leu
 370 375 380

gac tgg acg gtt gag ggg cca aaa cta cgc gac cgt att ttt gcg tac 1200
 Asp Trp Thr Val Glu Gly Pro Lys Leu Arg Asp Arg Ile Phe Ala Tyr
 385 390 395 400

ctt gag cag cat tac atg cct ggc tta cgg agt cag ctg gtc acg cac 1248
 Leu Glu Gln His Tyr Met Pro Gly Leu Arg Ser Gln Leu Val Thr His
 405 410 415

cgg atg ttt acg ccg ttt gat ttt cgc gac cag ctt aat gcc tat cat 1296
 Arg Met Phe Thr Pro Phe Asp Phe Arg Asp Gln Leu Asn Ala Tyr His
 420 425 430

ggc tca gcc ttt tct gtg gag ccc gtt ctt acc cag agc gcc tgg ttt 1344
 Gly Ser Ala Phe Ser Val Glu Pro Val Leu Thr Gln Ser Ala Trp Phe
 435 440 445

cgg ccg cat aac cgc gat aaa acc att act aat ctc tac ctg gtc ggc 1392
 Arg Pro His Asn Arg Asp Lys Thr Ile Thr Asn Leu Tyr Leu Val Gly
 450 455 460

gca ggc acg cat ccc ggc gca ggc att cct ggc gtc atc ggc tcg gca 1440
 Ala Gly Thr His Pro Gly Ala Gly Ile Pro Gly Val Ile Gly Ser Ala
 465 470 475 480

aaa gcg aca gca ggt ttg atg ctg gag gat ctg ata tga 1479
 Lys Ala Thr Ala Gly Leu Met Leu Glu Asp Leu Ile
 485 490

<210> 118

<211> 492

<212> PRT

<213> Erwinia uredovora

<400> 118

Met Lys Pro Thr Thr Val Ile Gly Ala Gly Phe Gly Gly Leu Ala Leu
 1 5 10 15

Ala Ile Arg Leu Gln Ala Ala Gly Ile Pro Val Leu Leu Leu Glu Gln
 20 25 30

Arg Asp Lys Pro Gly Gly Arg Ala Tyr Val Tyr Glu Asp Gln Gly Phe
 35 40 45

Thr Phe Asp Ala Gly Pro Thr Val Ile Thr Asp Pro Ser Ala Ile Glu
 50 55 60

Glu Leu Phe Ala Leu Ala Gly Lys Gln Leu Lys Glu Tyr Val Glu Leu

65

70

75

80

Leu Pro Val Thr Pro Phe Tyr Arg Leu Cys Trp Glu Ser Gly Lys Val
 85 90 95

Phe Asn Tyr Asp Asn Asp Gln Thr Arg Leu Glu Ala Gln Ile Gln Gln
 100 105 110

Phe Asn Pro Arg Asp Val Glu Gly Tyr Arg Gln Phe Leu Asp Tyr Ser
 115 120 125

Arg Ala Val Phe Lys Glu Gly Tyr Leu Lys Leu Gly Thr Val Pro Phe
 130 135 140

Leu Ser Phe Arg Asp Met Leu Arg Ala Ala Pro Gln Leu Ala Lys Leu
 145 150 155 160

Gln Ala Trp Arg Ser Val Tyr Ser Lys Val Ala Ser Tyr Ile Glu Asp
 165 170 175

Glu His Leu Arg Gln Ala Phe Ser Phe His Ser Leu Leu Val Gly Gly
 180 185 190

Asn Pro Phe Ala Thr Ser Ser Ile Tyr Thr Leu Ile His Ala Leu Glu
 195 200 205

Arg Glu Trp Gly Val Trp Phe Pro Arg Gly Gly Thr Gly Ala Leu Val
 210 215 220

Gln Gly Met Ile Lys Leu Phe Gln Asp Leu Gly Gly Glu Val Val Leu
 225 230 235 240

Asn Ala Arg Val Ser His Met Glu Thr Thr Gly Asn Lys Ile Glu Ala
 245 250 255

Val His Leu Glu Asp Gly Arg Arg Phe Leu Thr Gln Ala Val Ala Ser
 260 265 270

Asn Ala Asp Val Val His Thr Tyr Arg Asp Leu Leu Ser Gln His Pro
 275 280 285

Ala Ala Val Lys Gln Ser Asn Lys Leu Gln Thr Lys Arg Met Ser Asn
 290 295 300

Ser Leu Phe Val Leu Tyr Phe Gly Leu Asn His His His Asp Gln Leu

305 310 315 320
 Ala His His Thr Val Cys Phe Gly Pro Arg Tyr Arg Glu Leu Ile Asp
 325 330 335
 Glu Ile Phe Asn His Asp Gly Leu Ala Glu Asp Phe Ser Leu Tyr Leu
 340 345 350
 His Ala Pro Cys Val Thr Asp Ser Ser Leu Ala Pro Glu Gly Cys Gly
 355 360 365
 Ser Tyr Tyr Val Leu Ala Pro Val Pro His Leu Gly Thr Ala Asn Leu
 370 375 380
 Asp Trp Thr Val Glu Gly Pro Lys Leu Arg Asp Arg Ile Phe Ala Tyr
 385 390 395 400
 Leu Glu Gln His Tyr Met Pro Gly Leu Arg Ser Gln Leu Val Thr His
 405 410 415
 Arg Met Phe Thr Pro Phe Asp Phe Arg Asp Gln Leu Asn Ala Tyr His
 420 425 430
 Gly Ser Ala Phe Ser Val Glu Pro Val Leu Thr Gln Ser Ala Trp Phe
 435 440 445
 Arg Pro His Asn Arg Asp Lys Thr Ile Thr Asn Leu Tyr Leu Val Gly
 450 455 460
 Ala Gly Thr His Pro Gly Ala Gly Ile Pro Gly Val Ile Gly Ser Ala
 465 470 475 480
 Lys Ala Thr Ala Gly Leu Met Leu Glu Asp Leu Ile
 485 490

<210> 119

<211> 1725

<212> DNA

<213> Narcissus pseudonarcissus

<220>

<221> CDS

<400> 119

atg gct tct tcc act tgt tta att cat tct tcc tct ttt ggg gtt gga Met Ala Ser Ser Thr Cys Leu Ile His Ser Ser Ser Phe Gly Val Gly 1 5 10 15	48
gga aag aaa gtg aag atg aac acg atg att cga tcg aag ttg ttt tca Gly Lys Lys Val Lys Met Asn Thr Met Ile Arg Ser Lys Leu Phe Ser 20 25 30	96
att cgg tcg gct ttg gac act aag gtg tct gat atg agc gtc aat gct Ile Arg Ser Ala Leu Asp Thr Lys Val Ser Asp Met Ser Val Asn Ala 35 40 45	144
cca aaa gga ttg ttt cca cca gag cct gag cac tac agg ggg cca aag Pro Lys Gly Leu Phe Pro Pro Glu Pro Glu His Tyr Arg Gly Pro Lys 50 55 60	192
ctt aaa gtg gct atc att gga gct ggg ctc gct ggc atg tca act gca Leu Lys Val Ala Ile Ile Gly Ala Gly Leu Ala Gly Met Ser Thr Ala 65 70 75 80	240
gtg gag ctt ttg gat caa ggg cat gag gtt gac ata tat gaa tcc aga Val Glu Leu Leu Asp Gln Gly His Glu Val Asp Ile Tyr Glu Ser Arg 85 90 95	288
caa ttt att ggt ggt aaa gtc ggt tct ttt gta gat aag cgt gga aac Gln Phe Ile Gly Gly Lys Val Gly Ser Phe Val Asp Lys Arg Gly Asn 100 105 110	336
cat att gaa atg gga ctc cat gtg ttt ttt ggt tgc tat aac aat ctt His Ile Glu Met Gly Leu His Val Phe Phe Gly Cys Tyr Asn Asn Leu 115 120 125	384
ttc aga ctt atg aaa aag gta ggt gca gat gaa aat tta ctg gtg aag Phe Arg Leu Met Lys Lys Val Gly Ala Asp Glu Asn Leu Leu Val Lys 130 135 140	432
gat cat act cat acc ttt gta aac cga ggt gga gaa att ggt gaa ctt Asp His Thr His Thr Phe Val Asn Arg Gly Gly Glu Ile Gly Glu Leu 145 150 155 160	480
gat ttc cga ctt ccg atg ggt gca cca tta cat ggt att cgt gca ttt Asp Phe Arg Leu Pro Met Gly Ala Pro Leu His Gly Ile Arg Ala Phe 165 170 175	528
cta aca act aat caa ctg aag cct tat gat aaa gca agg aat gct gtg Leu Thr Thr Asn Gln Leu Lys Pro Tyr Asp Lys Ala Arg Asn Ala Val 180 185 190	576
gct ctt gcc ctt agc cca gtt gta cgt gct ctt att gat cca aat ggt Ala Leu Ala Leu Ser Pro Val Val Arg Ala Leu Ile Asp Pro Asn Gly 195 200 205	624
gca atg cag gat ata agg aac tta gat aat att agc ttt tct gat tgg Ala Met Gln Asp Ile Arg Asn Leu Asp Asn Ile Ser Phe Ser Asp Trp 210 215 220	672
ttc tta tcc aaa ggc ggt acc cgc atg agc atc caa agg atg tgg gat Phe Leu Ser Lys Gly Gly Thr Arg Met Ser Ile Gln Arg Met Trp Asp 225 230 235 240	720

cca gtt gct tat gcc ctc gga ttt att gac tgt gat aat atc agt gcc Pro Val Ala Tyr Ala Leu Gly Phe Ile Asp Cys Asp Asn Ile Ser Ala 245 250 255	768
cgt tgt atg ctt act ata ttt tct cta ttt gct act aag aca gaa gct Arg Cys Met Leu Thr Ile Phe Ser Leu Phe Ala Thr Lys Thr Glu Ala 260 265 270	816
tct ctg ttg cgt atg ttg aag ggt tct cct gat gtt tac tta agc ggt Ser Leu Leu Arg Met Leu Lys Gly Ser Pro Asp Val Tyr Leu Ser Gly 275 280 285	864
cct ata aga aag tat att aca gat aaa ggt gga agg ttt cac cta agg Pro Ile Arg Lys Tyr Ile Thr Asp Lys Gly Gly Arg Phe His Leu Arg 290 295 300	912
tgg ggg tgt aga gag ata ctt tat gat gaa cta tca aat ggc gac aca Trp Gly Cys Arg Glu Ile Leu Tyr Asp Glu Leu Ser Asn Gly Asp Thr 305 310 315 320	960
tat atc aca ggc att gca atg tct aag gct acc aat aaa aaa ctt gtg Tyr Ile Thr Gly Ile Ala Met Ser Lys Ala Thr Asn Lys Lys Leu Val 325 330 335	1008
aaa gct gac gtg tat gtt gca gca tgt gat gtt cct gga ata aaa agg Lys Ala Asp Val Tyr Val Ala Ala Cys Asp Val Pro Gly Ile Lys Arg 340 345 350	1056
ttg atc cca tct gag tgg aga gaa tgg gat cta ttt gac aat atc tat Leu Ile Pro Ser Glu Trp Arg Glu Trp Asp Leu Phe Asp Asn Ile Tyr 355 360 365	1104
aaa cta gtt gga gtt cca gtt gtc act gtt cag ctt agg tac aat ggt Lys Leu Val Gly Val Pro Val Val Thr Val Gln Leu Arg Tyr Asn Gly 370 375 380	1152
tgg gtg aca gag atg caa gat ctg gaa aaa tca agg cag ttg aga gct Trp Val Thr Glu Met Gln Asp Leu Glu Lys Ser Arg Gln Leu Arg Ala 385 390 395 400	1200
gca gta gga ttg gat aat ctt ctt tat act cca gat gca gac ttt tct Ala Val Gly Leu Asp Asn Leu Leu Tyr Thr Pro Asp Ala Asp Phe Ser 405 410 415	1248
tgt ttt tct gat ctt gca ctc tct tct cct gaa gat tat tat att gaa Cys Phe Ser Asp Leu Ala Leu Ser Ser Pro Glu Asp Tyr Tyr Ile Glu 420 425 430	1296
gga caa ggg tcc cta ata cag gct gtt ctc acg cca ggg gat cca tac Gly Gln Gly Ser Leu Ile Gln Ala Val Leu Thr Pro Gly Asp Pro Tyr 435 440 445	1344
atg ccc cta cct aat gat gca att ata gaa aga gtt cgg aaa cag gtt Met Pro Leu Pro Asn Asp Ala Ile Ile Glu Arg Val Arg Lys Gln Val 450 455 460	1392
ttg gat tta ttc cca tcc tct caa ggc ctg gaa gtt cta tgg tct tct Leu Asp Leu Phe Pro Ser Ser Gln Gly Leu Glu Val Leu Trp Ser Ser 465 470 475 480	1440

gtg gtt aaa atc gga caa tcc cta tat cgg gag ggg cct gga aag gac 1488
 Val Val Lys Ile Gly Gln Ser Leu Tyr Arg Glu Gly Pro Gly Lys Asp
 485 490 495

cca ttc aga cct gat cag aag aca cca gta aaa aat ttc ttc ctt gca 1536
 Pro Phe Arg Pro Asp Gln Lys Thr Pro Val Lys Asn Phe Phe Leu Ala
 500 505 510

ggc tca tac acc aaa cag gat tac att gac agt atg gaa gga gcg acc 1584
 Gly Ser Tyr Thr Lys Gln Asp Tyr Ile Asp Ser Met Glu Gly Ala Thr
 515 520 525

cta tcg ggg aga caa gca gct gca tat atc tgc agc gcc ggt gaa gat 1632
 Leu Ser Gly Arg Gln Ala Ala Ala Tyr Ile Cys Ser Ala Gly Glu Asp
 530 535 540

ctg gca gca ctt cgc aag aag atc gct gct gat cat cca gag caa ctg 1680
 Leu Ala Ala Leu Arg Lys Lys Ile Ala Ala Asp His Pro Glu Gln Leu
 545 550 555 560

atc aac aaa gat tct aac gtg tcg gat gaa ctg agt ctc gta taa 1725
 Ile Asn Lys Asp Ser Asn Val Ser Asp Glu Leu Ser Leu Val
 565 570

<210> 120

<211> 574

<212> PRT

<213> Narcissus pseudonarcissus

<400> 120

Met Ala Ser Ser Thr Cys Leu Ile His Ser Ser Ser Phe Gly Val Gly
 1 5 10 15

Gly Lys Lys Val Lys Met Asn Thr Met Ile Arg Ser Lys Leu Phe Ser
 20 25 30

Ile Arg Ser Ala Leu Asp Thr Lys Val Ser Asp Met Ser Val Asn Ala
 35 40 45

Pro Lys Gly Leu Phe Pro Pro Glu Pro Glu His Tyr Arg Gly Pro Lys
 50 55 60

Leu Lys Val Ala Ile Ile Gly Ala Gly Leu Ala Gly Met Ser Thr Ala
 65 70 75 80

Val Glu Leu Leu Asp Gln Gly His Glu Val Asp Ile Tyr Glu Ser Arg
 85 90 95

Gln Phe Ile Gly Gly Lys Val Gly Ser Phe Val Asp Lys Arg Gly Asn

100					105					110					
His	Ile	Glu	Met	Gly	Leu	His	Val	Phe	Phe	Gly	Cys	Tyr	Asn	Asn	Leu
	115						120					125			
Phe	Arg	Leu	Met	Lys	Lys	Val	Gly	Ala	Asp	Glu	Asn	Leu	Leu	Val	Lys
	130						135				140				
Asp	His	Thr	His	Thr	Phe	Val	Asn	Arg	Gly	Gly	Glu	Ile	Gly	Glu	Leu
145					150					155					160
Asp	Phe	Arg	Leu	Pro	Met	Gly	Ala	Pro	Leu	His	Gly	Ile	Arg	Ala	Phe
				165					170					175	
Leu	Thr	Thr	Asn	Gln	Leu	Lys	Pro	Tyr	Asp	Lys	Ala	Arg	Asn	Ala	Val
			180						185					190	
Ala	Leu	Ala	Leu	Ser	Pro	Val	Val	Arg	Ala	Leu	Ile	Asp	Pro	Asn	Gly
	195						200					205			
Ala	Met	Gln	Asp	Ile	Arg	Asn	Leu	Asp	Asn	Ile	Ser	Phe	Ser	Asp	Trp
	210					215					220				
Phe	Leu	Ser	Lys	Gly	Gly	Thr	Arg	Met	Ser	Ile	Gln	Arg	Met	Trp	Asp
225					230					235					240
Pro	Val	Ala	Tyr	Ala	Leu	Gly	Phe	Ile	Asp	Cys	Asp	Asn	Ile	Ser	Ala
				245					250					255	
Arg	Cys	Met	Leu	Thr	Ile	Phe	Ser	Leu	Phe	Ala	Thr	Lys	Thr	Glu	Ala
		260						265						270	
Ser	Leu	Leu	Arg	Met	Leu	Lys	Gly	Ser	Pro	Asp	Val	Tyr	Leu	Ser	Gly
	275						280					285			
Pro	Ile	Arg	Lys	Tyr	Ile	Thr	Asp	Lys	Gly	Gly	Arg	Phe	His	Leu	Arg
	290					295					300				
Trp	Gly	Cys	Arg	Glu	Ile	Leu	Tyr	Asp	Glu	Leu	Ser	Asn	Gly	Asp	Thr
305					310					315					320
Tyr	Ile	Thr	Gly	Ile	Ala	Met	Ser	Lys	Ala	Thr	Asn	Lys	Lys	Leu	Val
			325						330					335	

Lys Ala Asp Val Tyr Val Ala Ala Cys Asp Val Pro Gly Ile Lys Arg
 340 345 350

Leu Ile Pro Ser Glu Trp Arg Glu Trp Asp Leu Phe Asp Asn Ile Tyr
 355 360 365

Lys Leu Val Gly Val Pro Val Val Thr Val Gln Leu Arg Tyr Asn Gly
 370 375 380

Trp Val Thr Glu Met Gln Asp Leu Glu Lys Ser Arg Gln Leu Arg Ala
 385 390 395 400

Ala Val Gly Leu Asp Asn Leu Leu Tyr Thr Pro Asp Ala Asp Phe Ser
 405 410 415

Cys Phe Ser Asp Leu Ala Leu Ser Ser Pro Glu Asp Tyr Tyr Ile Glu
 420 425 430

Gly Gln Gly Ser Leu Ile Gln Ala Val Leu Thr Pro Gly Asp Pro Tyr
 435 440 445

Met Pro Leu Pro Asn Asp Ala Ile Ile Glu Arg Val Arg Lys Gln Val
 450 455 460

Leu Asp Leu Phe Pro Ser Ser Gln Gly Leu Glu Val Leu Trp Ser Ser
 465 470 475 480

Val Val Lys Ile Gly Gln Ser Leu Tyr Arg Glu Gly Pro Gly Lys Asp
 485 490 495

Pro Phe Arg Pro Asp Gln Lys Thr Pro Val Lys Asn Phe Phe Leu Ala
 500 505 510

Gly Ser Tyr Thr Lys Gln Asp Tyr Ile Asp Ser Met Glu Gly Ala Thr
 515 520 525

Leu Ser Gly Arg Gln Ala Ala Ala Tyr Ile Cys Ser Ala Gly Glu Asp
 530 535 540

Leu Ala Ala Leu Arg Lys Lys Ile Ala Ala Asp His Pro Glu Gln Leu
 545 550 555 560

Ile Asn Lys Asp Ser Asn Val Ser Asp Glu Leu Ser Leu Val
 565 570

<210> 121

<211> 1848

<212> DNA

<213> Lycopersicon esculentum

<220>

<221> CDS

<400> 121

atg tgt acc ttg agt ttt atg tat cct aat tca ctt ctt gat ggt acc	48
Met Cys Thr Leu Ser Phe Met Tyr Pro Asn Ser Leu Leu Asp Gly Thr	
1 5 10 15	
tgc aag act gta gct ttg ggt gat agc aaa cca aga tac aat aaa cag	96
Cys Lys Thr Val Ala Leu Gly Asp Ser Lys Pro Arg Tyr Asn Lys Gln	
20 25 30	
aga agt tct tgt ttt gac cct ttg ata att gga aat tgt act gat cag	144
Arg Ser Ser Cys Phe Asp Pro Leu Ile Ile Gly Asn Cys Thr Asp Gln	
35 40 45	
cag cag ctt tgt ggc ttg agt tgg ggg gtg gac aag gct aag gga aga	192
Gln Gln Leu Cys Gly Leu Ser Trp Gly Val Asp Lys Ala Lys Gly Arg	
50 55 60	
aga ggg ggt act gtt tcc aat ttg aaa gca gtt gta gat gta gac aaa	240
Arg Gly Gly Thr Val Ser Asn Leu Lys Ala Val Val Asp Val Asp Lys	
65 70 75 80	
aga gtg gag agc tat ggc agt agt gat gta gaa gga aat gag agt ggc	288
Arg Val Glu Ser Tyr Gly Ser Ser Asp Val Glu Gly Asn Glu Ser Gly	
85 90 95	
agc tat gat gcc att gtt ata ggt tca gga ata ggt gga ttg gtg gca	336
Ser Tyr Asp Ala Ile Val Ile Gly Ser Gly Ile Gly Gly Leu Val Ala	
100 105 110	
gcg acg cag ctg gcg gtt aag gga gct aag gtt tta gtt ctg gag aag	384
Ala Thr Gln Leu Ala Val Lys Gly Ala Lys Val Leu Val Leu Glu Lys	
115 120 125	
tat gtt att cct ggt gga agc tct ggc ttt tac gag agg gat ggt tat	432
Tyr Val Ile Pro Gly Gly Ser Ser Gly Phe Tyr Glu Arg Asp Gly Tyr	
130 135 140	
aag ttt gat gtt ggt tca tca gtg atg ttt gga ttc agt gat aag gga	480
Lys Phe Asp Val Gly Ser Ser Val Met Phe Gly Phe Ser Asp Lys Gly	
145 150 155 160	
aac ctc aat tta att act caa gca ttg gca gca gta gga cgt aaa tta	528
Asn Leu Asn Leu Ile Thr Gln Ala Leu Ala Ala Val Gly Arg Lys Leu	
165 170 175	
gaa gtt ata cct gac cca aca act gta cat ttc cac ctg cca aat gac	576
Glu Val Ile Pro Asp Pro Thr Thr Val His Phe His Leu Pro Asn Asp	
180 185 190	

ctt tct gtt cgt ata cac cga gag tat gat gac ttc att gaa gag ctt Leu Ser Val Arg Ile His Arg Glu Tyr Asp Asp Phe Ile Glu Glu Leu 195 200 205	624
gtg agt aaa ttt cca cat gaa aag gaa ggg att atc aaa ttt tac agt Val Ser Lys Phe Pro His Glu Lys Glu Gly Ile Ile Lys Phe Tyr Ser 210 215 220	672
gaa tgc tgg aag atc ttt aat tct ctg aat tca ttg gaa ctg aag tct Glu Cys Trp Lys Ile Phe Asn Ser Leu Asn Ser Leu Glu Leu Lys Ser 225 230 235 240	720
ttg gag gaa ccc atc tac ctt ttt ggc cag ttc ttt aag aag ccc ctt Leu Glu Glu Pro Ile Tyr Leu Phe Gly Gln Phe Phe Lys Lys Pro Leu 245 250 255	768
gaa tgc ttg act ctt gcc tac tat ttg ccc cag aat gct ggt agc atc Glu Cys Leu Thr Leu Ala Tyr Tyr Leu Pro Gln Asn Ala Gly Ser Ile 260 265 270	816
gct cgg aag tat ata aga gat cct ggg ttg ctg tct ttt ata gat gca Ala Arg Lys Tyr Ile Arg Asp Pro Gly Leu Leu Ser Phe Ile Asp Ala 275 280 285	864
gag tgc ttt atc gtg agt aca gtt aat gca tta caa aca cca atg atc Glu Cys Phe Ile Val Ser Thr Val Asn Ala Leu Gln Thr Pro Met Ile 290 295 300	912
aat gca agc atg gtt cta tgt gac aga cat ttt ggc gga atc aac tac Asn Ala Ser Met Val Leu Cys Asp Arg His Phe Gly Gly Ile Asn Tyr 305 310 315 320	960
ccc gtt ggt gga gtt ggc gag atc gcc aaa tcc tta gca aaa ggc ttg Pro Val Gly Gly Val Gly Glu Ile Ala Lys Ser Leu Ala Lys Gly Leu 325 330 335	1008
gat gat cac gga agt cag ata ctt tat agg gca aat gtt aca agt atc Asp Asp His Gly Ser Gln Ile Leu Tyr Arg Ala Asn Val Thr Ser Ile 340 345 350	1056
att ttg gac aat ggc aaa gct gtg gga gtg aag ctt tct gac ggg agg Ile Leu Asp Asn Gly Lys Ala Val Gly Val Lys Leu Ser Asp Gly Arg 355 360 365	1104
aag ttt tat gct aaa acc ata gta tcg aat gct acc aga tgg gat act Lys Phe Tyr Ala Lys Thr Ile Val Ser Asn Ala Thr Arg Trp Asp Thr 370 375 380	1152
ttt gga aag ctt tta aaa gct gag aat ctg cca aaa gaa gaa gaa aat Phe Gly Lys Leu Leu Lys Ala Glu Asn Leu Pro Lys Glu Glu Glu Asn 385 390 395 400	1200
ttc cag aaa gct tat gta aaa gca cct tct ttt ctt tct att cat atg Phe Gln Lys Ala Tyr Val Lys Ala Pro Ser Phe Leu Ser Ile His Met 405 410 415	1248
gga gtt aaa gca gat gta ctc cca cca gac aca gat tgt cac cat ttt Gly Val Lys Ala Asp Val Leu Pro Pro Asp Thr Asp Cys His His Phe 420 425 430	1296

gtc ctc gag gat gat tgg aca aat ttg gag aaa cca tat gga agt ata	1344
Val Leu Glu Asp Asp Trp Thr Asn Leu Glu Lys Pro Tyr Gly Ser Ile	
435 440 445	
ttc ttg agt att cca aca gtt ctt gat tcc tca ttg gcc cca gaa gga	1392
Phe Leu Ser Ile Pro Thr Val Leu Asp Ser Ser Leu Ala Pro Glu Gly	
450 455 460	
cac cat att ctt cac att ttt aca aca tcg agc att gaa gat tgg gag	1440
His His Ile Leu His Ile Phe Thr Thr Ser Ser Ile Glu Asp Trp Glu	
465 470 475 480	
gga ctc tct ccg aaa gac tat gaa gcg aag aaa gag gtt gtt gct gaa	1488
Gly Leu Ser Pro Lys Asp Tyr Glu Ala Lys Lys Glu Val Val Ala Glu	
485 490 495	
agg att ata agc aga ctt gaa aaa aca ctc ttc cca ggg ctt aag tca	1536
Arg Ile Ile Ser Arg Leu Glu Lys Thr Leu Phe Pro Gly Leu Lys Ser	
500 505 510	
tct att ctc ttt aag gag gtg gga act cca aag acc cac aga cga tac	1584
Ser Ile Leu Phe Lys Glu Val Gly Thr Pro Lys Thr His Arg Arg Tyr	
515 520 525	
ctt gct cgt gat agt ggt acc tat gga cca atg cca cgc gga aca cct	1632
Leu Ala Arg Asp Ser Gly Thr Tyr Gly Pro Met Pro Arg Gly Thr Pro	
530 535 540	
aag gga ctc ctg gga atg cct ttc aat acc act gct ata gat ggt cta	1680
Lys Gly Leu Leu Gly Met Pro Phe Asn Thr Thr Ala Ile Asp Gly Leu	
545 550 555 560	
tat tgt gtt ggc gat agt tgc ttc cca gga caa ggt gtt ata gct gta	1728
Tyr Cys Val Gly Asp Ser Cys Phe Pro Gly Gln Gly Val Ile Ala Val	
565 570 575	
gcc ttt tca gga gta atg tgc gct cat cgt gtt gca gct gac tta ggg	1776
Ala Phe Ser Gly Val Met Cys Ala His Arg Val Ala Ala Asp Leu Gly	
580 585 590	
ttt gaa aaa aaa tca gat gtg ctg gac agt gct ctt ctt aga cta ctt	1824
Phe Glu Lys Lys Ser Asp Val Leu Asp Ser Ala Leu Leu Arg Leu Leu	
595 600 605	
ggt tgg tta agg aca cta gca tga	1848
Gly Trp Leu Arg Thr Leu Ala	
610 615	

<210> 122

<211> 615

<212> PRT

<213> Lycopersicon esculentum

<400> 122

Met Cys Thr Leu Ser Phe Met Tyr Pro Asn Ser Leu Leu Asp Gly Thr
 1 5 10 15

Cys Lys Thr Val Ala Leu Gly Asp Ser Lys Pro Arg Tyr Asn Lys Gln
 20 25 30

Arg Ser Ser Cys Phe Asp Pro Leu Ile Ile Gly Asn Cys Thr Asp Gln
 35 40 45

Gln Gln Leu Cys Gly Leu Ser Trp Gly Val Asp Lys Ala Lys Gly Arg
 50 55 60

Arg Gly Gly Thr Val Ser Asn Leu Lys Ala Val Val Asp Val Asp Lys
 65 70 75 80

Arg Val Glu Ser Tyr Gly Ser Ser Asp Val Glu Gly Asn Glu Ser Gly
 85 90 95

Ser Tyr Asp Ala Ile Val Ile Gly Ser Gly Ile Gly Gly Leu Val Ala
 100 105 110

Ala Thr Gln Leu Ala Val Lys Gly Ala Lys Val Leu Val Leu Glu Lys
 115 120 125

Tyr Val Ile Pro Gly Gly Ser Ser Gly Phe Tyr Glu Arg Asp Gly Tyr
 130 135 140

Lys Phe Asp Val Gly Ser Ser Val Met Phe Gly Phe Ser Asp Lys Gly
 145 150 155 160

Asn Leu Asn Leu Ile Thr Gln Ala Leu Ala Ala Val Gly Arg Lys Leu
 165 170 175

Glu Val Ile Pro Asp Pro Thr Thr Val His Phe His Leu Pro Asn Asp
 180 185 190

Leu Ser Val Arg Ile His Arg Glu Tyr Asp Asp Phe Ile Glu Glu Leu
 195 200 205

Val Ser Lys Phe Pro His Glu Lys Glu Gly Ile Ile Lys Phe Tyr Ser
 210 215 220

Glu Cys Trp Lys Ile Phe Asn Ser Leu Asn Ser Leu Glu Leu Lys Ser
 225 230 235 240

Leu Glu Glu Pro Ile Tyr Leu Phe Gly Gln Phe Phe Lys Lys Pro Leu
 245 250 255

Glu Cys Leu Thr Leu Ala Tyr Tyr Leu Pro Gln Asn Ala Gly Ser Ile
 260 265 270

Ala Arg Lys Tyr Ile Arg Asp Pro Gly Leu Leu Ser Phe Ile Asp Ala
 275 280 285

Glu Cys Phe Ile Val Ser Thr Val Asn Ala Leu Gln Thr Pro Met Ile
 290 295 300

Asn Ala Ser Met Val Leu Cys Asp Arg His Phe Gly Gly Ile Asn Tyr
 305 310 315 320

Pro Val Gly Gly Val Gly Glu Ile Ala Lys Ser Leu Ala Lys Gly Leu
 325 330 335

Asp Asp His Gly Ser Gln Ile Leu Tyr Arg Ala Asn Val Thr Ser Ile
 340 345 350

Ile Leu Asp Asn Gly Lys Ala Val Gly Val Lys Leu Ser Asp Gly Arg
 355 360 365

Lys Phe Tyr Ala Lys Thr Ile Val Ser Asn Ala Thr Arg Trp Asp Thr
 370 375 380

Phe Gly Lys Leu Leu Lys Ala Glu Asn Leu Pro Lys Glu Glu Glu Asn
 385 390 395 400

Phe Gln Lys Ala Tyr Val Lys Ala Pro Ser Phe Leu Ser Ile His Met
 405 410 415

Gly Val Lys Ala Asp Val Leu Pro Pro Asp Thr Asp Cys His His Phe
 420 425 430

Val Leu Glu Asp Asp Trp Thr Asn Leu Glu Lys Pro Tyr Gly Ser Ile
 435 440 445

Phe Leu Ser Ile Pro Thr Val Leu Asp Ser Ser Leu Ala Pro Glu Gly
 450 455 460

His His Ile Leu His Ile Phe Thr Thr Ser Ser Ile Glu Asp Trp Glu
 465 470 475 480

Gly Leu Ser Pro Lys Asp Tyr Glu Ala Lys Lys Glu Val Val Ala Glu
 485 490 495

Arg Ile Ile Ser Arg Leu Glu Lys Thr Leu Phe Pro Gly Leu Lys Ser
 500 505 510

Ser Ile Leu Phe Lys Glu Val Gly Thr Pro Lys Thr His Arg Arg Tyr
 515 520 525

Leu Ala Arg Asp Ser Gly Thr Tyr Gly Pro Met Pro Arg Gly Thr Pro
 530 535 540

Lys Gly Leu Leu Gly Met Pro Phe Asn Thr Thr Ala Ile Asp Gly Leu
 545 550 555 560

Tyr Cys Val Gly Asp Ser Cys Phe Pro Gly Gln Gly Val Ile Ala Val
 565 570 575

Ala Phe Ser Gly Val Met Cys Ala His Arg Val Ala Ala Asp Leu Gly
 580 585 590

Phe Glu Lys Lys Ser Asp Val Leu Asp Ser Ala Leu Leu Arg Leu Leu
 595 600 605

Gly Trp Leu Arg Thr Leu Ala
 610 615

<210> 123

<211> 1233

<212> DNA

<213> Tagetes erecta

<220>

<221> CDS

<400> 123

atg gcc aca cac aaa ctc ctt caa ttc acc acc aat ctc cca cca tct 48
 Met Ala Thr His Lys Leu Leu Gln Phe Thr Thr Asn Leu Pro Pro Ser
 1 5 10 15

tct tct tca atc tct act ggc tgt tca ctc tcc ccc ttc ttc ctc aaa 96
 Ser Ser Ser Ile Ser Thr Gly Cys Ser Leu Ser Pro Phe Phe Leu Lys
 20 25 30

tca tct tct cat tcc cct aac cct cgc cga cac cgc cgc tcc gcc gta 144
 Ser Ser Ser His Ser Pro Asn Pro Arg Arg His Arg Arg Ser Ala Val
 35 40 45

tgc tgc tct ttc gcc tca ctc gac tct gca aaa atc aaa gtc gtt ggc Cys Cys Ser Phe Ala Ser Leu Asp Ser Ala Lys Ile Lys Val Val Gly 50 55 60	192
gtc ggt ggt ggt ggc aac aat gcc gtt aac cgc atg att ggt agc ggc Val Gly Gly Gly Gly Asn Asn Ala Val Asn Arg Met Ile Gly Ser Gly 65 70 75 80	240
tta cag ggt gtt gat ttt tac gcc att aac acg gac tca caa gcg ctt Leu Gln Gly Val Asp Phe Tyr Ala Ile Asn Thr Asp Ser Gln Ala Leu 85 90 95	288
ctg caa tct gtt gca cat aac cct att caa att ggg gag ctt ttg act Leu Gln Ser Val Ala His Asn Pro Ile Gln Ile Gly Glu Leu Leu Thr 100 105 110	336
cgt gga tta ggt act ggt ggg aac ccg ctt ttg gga gaa cag gct gcg Arg Gly Leu Gly Thr Gly Gly Asn Pro Leu Leu Gly Glu Gln Ala Ala 115 120 125	384
gag gag tcg aag gaa gcg att ggg aat gcg ctt aaa ggg tcg gat ctt Glu Glu Ser Lys Glu Ala Ile Gly Asn Ala Leu Lys Gly Ser Asp Leu 130 135 140	432
gtg ttt ata aca gca ggt atg ggt ggt ggg acg ggt tcg ggt gct gct Val Phe Ile Thr Ala Gly Met Gly Gly Gly Thr Gly Ser Gly Ala Ala 145 150 155 160	480
cca gtt gta gcg cag ata gcg aaa gaa gca ggg tat tta act gtt ggt Pro Val Val Ala Gln Ile Ala Lys Glu Ala Gly Tyr Leu Thr Val Gly 165 170 175	528
gtt gta acg tac cca ttc agc ttt gaa ggc cgt aaa aga tca gta cag Val Val Thr Tyr Pro Phe Ser Phe Glu Gly Arg Lys Arg Ser Val Gln 180 185 190	576
gcg tta gag gct att gag aag ctg caa aag aac gtt gac aca ctt ata Ala Leu Glu Ala Ile Glu Lys Leu Gln Lys Asn Val Asp Thr Leu Ile 195 200 205	624
gtg att cca aat gac cgt ttg ctg gat att gct gat gaa aac acg cct Val Ile Pro Asn Asp Arg Leu Leu Asp Ile Ala Asp Glu Asn Thr Pro 210 215 220	672
ctt cag gat gct ttt ctt ctt gct gat gat gta ctc cgc caa gga gtt Leu Gln Asp Ala Phe Leu Leu Ala Asp Asp Val Leu Arg Gln Gly Val 225 230 235 240	720
caa gga atc tca gat ata att aca ata cct ggg ctg gta aat gtg gac Gln Gly Ile Ser Asp Ile Ile Thr Ile Pro Gly Leu Val Asn Val Asp 245 250 255	768
ttt gca gac gtt aaa gca gtc atg aaa gat tct gga act gca atg ctt Phe Ala Asp Val Lys Ala Val Met Lys Asp Ser Gly Thr Ala Met Leu 260 265 270	816
ggt gtc ggt gtt tcc tca agt aaa aac cga gct gaa gaa gca gct gaa Gly Val Gly Val Ser Ser Ser Lys Asn Arg Ala Glu Glu Ala Ala Glu 275 280 285	864

caa gca act ctt gct cct ttg att gga tca tca att caa tct gct aca 912
 Gln Ala Thr Leu Ala Pro Leu Ile Gly Ser Ser Ile Gln Ser Ala Thr
 290 295 300

ggt gtt gtt tat aat att acc gga ggg aag gac ata act cta caa gaa 960
 Gly Val Val Tyr Asn Ile Thr Gly Gly Lys Asp Ile Thr Leu Gln Glu
 305 310 315 320

gtc aac agg gtt tct cag gtg gta aca agt ttg gca gat cca tca gca 1008
 Val Asn Arg Val Ser Gln Val Val Thr Ser Leu Ala Asp Pro Ser Ala
 325 330 335

aac att ata ttc ggg gca gtg gta gat gag aga tac aac ggg gag att 1056
 Asn Ile Ile Phe Gly Ala Val Val Asp Glu Arg Tyr Asn Gly Glu Ile
 340 345 350

cat gtg acc att gtt gct act ggc ttt gcc cag tcg ttt cag aaa tct 1104
 His Val Thr Ile Val Ala Thr Gly Phe Ala Gln Ser Phe Gln Lys Ser
 355 360 365

ctt ctt gct gac ccg aaa gga gca aaa ctt gtt gat aga aat caa gaa 1152
 Leu Leu Ala Asp Pro Lys Gly Ala Lys Leu Val Asp Arg Asn Gln Glu
 370 375 380

cct aca caa cct ttg act tcc gcg aga tct ttg aca aca cct tct cct 1200
 Pro Thr Gln Pro Leu Thr Ser Ala Arg Ser Leu Thr Thr Pro Ser Pro
 385 390 395 400

gct ccg tct cgg tct agg aaa ctc ttc ttt taa 1233
 Ala Pro Ser Arg Ser Arg Lys Leu Phe Phe
 405 410

<210> 124

<211> 410

<212> PRT

<213> Tagetes erecta

<400> 124

Met Ala Thr His Lys Leu Leu Gln Phe Thr Thr Asn Leu Pro Pro Ser
 1 5 10 15

Ser Ser Ser Ile Ser Thr Gly Cys Ser Leu Ser Pro Phe Phe Leu Lys
 20 25 30

Ser Ser Ser His Ser Pro Asn Pro Arg Arg His Arg Arg Ser Ala Val
 35 40 45

Cys Cys Ser Phe Ala Ser Leu Asp Ser Ala Lys Ile Lys Val Val Gly
 50 55 60

Val Gly Gly Gly Gly Asn Asn Ala Val Asn Arg Met Ile Gly Ser Gly
65 70 75 80

Leu Gln Gly Val Asp Phe Tyr Ala Ile Asn Thr Asp Ser Gln Ala Leu
85 90 95

Leu Gln Ser Val Ala His Asn Pro Ile Gln Ile Gly Glu Leu Leu Thr
100 105 110

Arg Gly Leu Gly Thr Gly Gly Asn Pro Leu Leu Gly Glu Gln Ala Ala
115 120 125

Glu Glu Ser Lys Glu Ala Ile Gly Asn Ala Leu Lys Gly Ser Asp Leu
130 135 140

Val Phe Ile Thr Ala Gly Met Gly Gly Gly Thr Gly Ser Gly Ala Ala
145 150 155 160

Pro Val Val Ala Gln Ile Ala Lys Glu Ala Gly Tyr Leu Thr Val Gly
165 170 175

Val Val Thr Tyr Pro Phe Ser Phe Glu Gly Arg Lys Arg Ser Val Gln
180 185 190

Ala Leu Glu Ala Ile Glu Lys Leu Gln Lys Asn Val Asp Thr Leu Ile
195- 200 205

Val Ile Pro Asn Asp Arg Leu Leu Asp Ile Ala Asp Glu Asn Thr Pro
210 215 220

Leu Gln Asp Ala Phe Leu Leu Ala Asp Asp Val Leu Arg Gln Gly Val
225 230 235 240

Gln Gly Ile Ser Asp Ile Ile Thr Ile Pro Gly Leu Val Asn Val Asp
245 250 255

Phe Ala Asp Val Lys Ala Val Met Lys Asp Ser Gly Thr Ala Met Leu
260 265 270

Gly Val Gly Val Ser Ser Ser Lys Asn Arg Ala Glu Glu Ala Ala Glu
275 280 285

Gln Ala Thr Leu Ala Pro Leu Ile Gly Ser Ser Ile Gln Ser Ala Thr
290 295 300

Gly Val Val Tyr Asn Ile Thr Gly Gly Lys Asp Ile Thr Leu Gln Glu
305 310 315 320

Val Asn Arg Val Ser Gln Val Val Thr Ser Leu Ala Asp Pro Ser Ala
325 330 335

Asn Ile Ile Phe Gly Ala Val Val Asp Glu Arg Tyr Asn Gly Glu Ile
340 345 350

His Val Thr Ile Val Ala Thr Gly Phe Ala Gln Ser Phe Gln Lys Ser
355 360 365

Leu Leu Ala Asp Pro Lys Gly Ala Lys Leu Val Asp Arg Asn Gln Glu
370 375 380

Pro Thr Gln Pro Leu Thr Ser Ala Arg Ser Leu Thr Thr Pro Ser Pro
385 390 395 400

Ala Pro Ser Arg Ser Arg Lys Leu Phe Phe
405 410

<210> 125

<211> 891

<212> DNA

<213> Tagetes erecta

<220>

<221> CDS

<400> 125

atg aca tcc ctg agg ttt cta aca gaa ccc tca ctt gta tgc tca tcc 48
Met Thr Ser Leu Arg Phe Leu Thr Glu Pro Ser Leu Val Cys Ser Ser
1 5 10 15

act ttc ccc aca ttc aat ccc cta cac aaa acc cta act aaa cca aca 96
Thr Phe Pro Thr Phe Asn Pro Leu His Lys Thr Leu Thr Lys Pro Thr
20 25 30

cca aaa ccc tac cca aag cca cca cca att cgc tcc gtc ctt caa tac 144
Pro Lys Pro Tyr Pro Lys Pro Pro Pro Ile Arg Ser Val Leu Gln Tyr
35 40 45

aat cgc aaa cca gag ctc gcc gga gac act cca cga gtc gtc gca atc 192
Asn Arg Lys Pro Glu Leu Ala Gly Asp Thr Pro Arg Val Val Ala Ile
50 55 60

gac gcc gac gtt ggt cta cgt aac ctc gat ctt ctt ctc ggt ctc gaa 240
Asp Ala Asp Val Gly Leu Arg Asn Leu Asp Leu Leu Leu Gly Leu Glu

65	70	75	80	
aac cgc gtc aat tac acc gtc gtt gaa gtt ctc aac ggc gat tgc aga Asn Arg Val Asn Tyr Thr Val Val Glu Val Leu Asn Gly Asp Cys Arg	85	90	95	288
ctc gac caa gcc cta gtt cgt gat aaa cgc tgg tca aat ttc gaa ttg Leu Asp Gln Ala Leu Val Arg Asp Lys Arg Trp Ser Asn Phe Glu Leu	100	105	110	336
ctt tgt att tca aaa cct agg tca aaa ttg cct tta gga ttt ggg gga Leu Cys Ile Ser Lys Pro Arg Ser Lys Leu Pro Leu Gly Phe Gly Gly	115	120	125	384
aaa gct tta gtt tgg ctt gat gca tta aaa gat agg caa gaa ggt tgc Lys Ala Leu Val Trp Leu Asp Ala Leu Lys Asp Arg Gln Glu Gly Cys	130	135	140	432
ccg gat ttt ata ctt ata gat tgt cct gca ggt att gat gcc ggg ttc Pro Asp Phe Ile Leu Ile Asp Cys Pro Ala Gly Ile Asp Ala Gly Phe	145	150	155	480
ata acc gcc att aca ccg gct aac gaa gcc gta tta gtt aca aca cct Ile Thr Ala Ile Thr Pro Ala Asn Glu Ala Val Leu Val Thr Thr Pro	165	170	175	528
gat att act gca ttg aga gat gca gat aga gtt aca ggc ttg ctt gaa Asp Ile Thr Ala Leu Arg Asp Ala Asp Arg Val Thr Gly Leu Leu Glu	180	185	190	576
tgt gat gga att agg gat att aaa atg att gtg aac aga gtt aga act Cys Asp Gly Ile Arg Asp Ile Lys Met Ile Val Asn Arg Val Arg Thr	195	200	205	624
gat ttg ata agg ggt gaa gat atg atg tca gtt ctt gat gtt caa gag Asp Leu Ile Arg Gly Glu Asp Met Met Ser Val Leu Asp Val Gln Glu	210	215	220	672
atg ttg gga ttg tca ttg ttg agt gat acc cga gga ttc gaa gtg att Met Leu Gly Leu Ser Leu Leu Ser Asp Thr Arg Gly Phe Glu Val Ile	225	230	235	720
cgg agt acg aat aga ggg ttt ccg ctt gtg ttg aac aag cct ccg act Arg Ser Thr Asn Arg Gly Phe Pro Leu Val Leu Asn Lys Pro Pro Thr	245	250	255	768
tta gca gga ttg gca ttt gag cag gct gct tgg aga ttg gtt gag caa Leu Ala Gly Leu Ala Phe Glu Gln Ala Ala Trp Arg Leu Val Glu Gln	260	265	270	816
gat agc atg aag gct gtg atg gtg gag gaa gaa cct aaa aag agg gga Asp Ser Met Lys Ala Val Met Val Glu Glu Glu Pro Lys Lys Arg Gly	275	280	285	864
ttt ttc tcg ttt ttt gga ggt tag tga Phe Phe Ser Phe Phe Gly Gly	290	295		891

<211> 295

<212> PRT

<213> Tagetes erecta

<400> 126

Met Thr Ser Leu Arg Phe Leu Thr Glu Pro Ser Leu Val Cys Ser Ser
 1 5 10 15

Thr Phe Pro Thr Phe Asn Pro Leu His Lys Thr Leu Thr Lys Pro Thr
 20 25 30

Pro Lys Pro Tyr Pro Lys Pro Pro Pro Ile Arg Ser Val Leu Gln Tyr
 35 40 45

Asn Arg Lys Pro Glu Leu Ala Gly Asp Thr Pro Arg Val Val Ala Ile
 50 55 60

Asp Ala Asp Val Gly Leu Arg Asn Leu Asp Leu Leu Leu Gly Leu Glu
 65 70 75 80

Asn Arg Val Asn Tyr Thr Val Val Glu Val Leu Asn Gly Asp Cys Arg
 85 90 95

Leu Asp Gln Ala Leu Val Arg Asp Lys Arg Trp Ser Asn Phe Glu Leu
 100 105 110

Leu Cys Ile Ser Lys Pro Arg Ser Lys Leu Pro Leu Gly Phe Gly Gly
 115 120 125

Lys Ala Leu Val Trp Leu Asp Ala Leu Lys Asp Arg Gln Glu Gly Cys
 130 135 140

Pro Asp Phe Ile Leu Ile Asp Cys Pro Ala Gly Ile Asp Ala Gly Phe
 145 150 155 160

Ile Thr Ala Ile Thr Pro Ala Asn Glu Ala Val Leu Val Thr Thr Pro
 165 170 175

Asp Ile Thr Ala Leu Arg Asp Ala Asp Arg Val Thr Gly Leu Leu Glu
 180 185 190

Cys Asp Gly Ile Arg Asp Ile Lys Met Ile Val Asn Arg Val Arg Thr
 195 200 205

Asp Leu Ile Arg Gly Glu Asp Met Met Ser Val Leu Asp Val Gln Glu
 210 215 220

Met Leu Gly Leu Ser Leu Leu Ser Asp Thr Arg Gly Phe Glu Val Ile
 225 230 235 240

Arg Ser Thr Asn Arg Gly Phe Pro Leu Val Leu Asn Lys Pro Pro Thr
 245 250 255

Leu Ala Gly Leu Ala Phe Glu Gln Ala Ala Trp Arg Leu Val Glu Gln
 260 265 270

Asp Ser Met Lys Ala Val Met Val Glu Glu Glu Pro Lys Lys Arg Gly
 275 280 285

Phe Phe Ser Phe Phe Gly Gly
 290 295

<210> 127

<211> 332

<212> DNA

<213> Tagetes erecta

<220>

<221> CDS

<222> (1)..(330)

<400> 127

aag ctt gca cga gcc tct ctc tat ttt tac act tca atg gcg gca gca 48
 Lys Leu Ala Arg Ala Ser Leu Tyr Phe Tyr Thr Ser Met Ala Ala Ala
 1 5 10 15

att gct gtc cct tgt agc tca aga cca ttt ggc tta ggt cga atg cgg 96
 Ile Ala Val Pro Cys Ser Ser Arg Pro Phe Gly Leu Gly Arg Met Arg
 20 25 30

tta ctt ggt cat aaa ccc aca acc ata act tgt cac ttc ccc ttt tct 144
 Leu Leu Gly His Lys Pro Thr Thr Ile Thr Cys His Phe Pro Phe Ser
 35 40 45

ttt tct atc aaa tca ttt acc cca att gtt agg ggc aga aga tgt act 192
 Phe Ser Ile Lys Ser Phe Thr Pro Ile Val Arg Gly Arg Arg Cys Thr
 50 55 60

gtt tgt ttt gtt gcc ggt ggc gac agt aat agt aac agt aat aat aat 240
 Val Cys Phe Val Ala Gly Gly Asp Ser Asn Ser Asn Ser Asn Asn Asn
 65 70 75 80

agt gac agt aat agt aat aat ccg ggt ctg gat tta aac ccg gcg gtt 288
 Ser Asp Ser Asn Ser Asn Asn Pro Gly Leu Asp Leu Asn Pro Ala Val
 85 90 95

atg aac cgt aac cgt ttg gtt gaa gaa aaa atg gag agg tcg ac 332
 Met Asn Arg Asn Arg Leu Val Glu Glu Lys Met Glu Arg Ser
 100 105 110

<210> 128

<211> 110

<212> PRT

<213> Tagetes erecta

<400> 128

Lys Leu Ala Arg Ala Ser Leu Tyr Phe Tyr Thr Ser Met Ala Ala Ala
 1 5 10 15

Ile Ala Val Pro Cys Ser Ser Arg Pro Phe Gly Leu Gly Arg Met Arg
 20 25 30

Leu Leu Gly His Lys Pro Thr Thr Ile Thr Cys His Phe Pro Phe Ser
 35 40 45

Phe Ser Ile Lys Ser Phe Thr Pro Ile Val Arg Gly Arg Arg Cys Thr
 50 55 60

Val Cys Phe Val Ala Gly Gly Asp Ser Asn Ser Asn Ser Asn Asn Asn
 65 70 75 80

Ser Asp Ser Asn Ser Asn Asn Pro Gly Leu Asp Leu Asn Pro Ala Val
 85 90 95

Met Asn Arg Asn Arg Leu Val Glu Glu Lys Met Glu Arg Ser
 100 105 110

<210> 129

<211> 37

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 129

gcgcatgcat ctagaaatga tccagttaga acaacca

37

<210> 130

<211> 37

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 130

gcgcatgctc tagactatatt tgctttgtaa atttctg

37

<210> 131

<211> 792

<212> DNA

<213> Nostoc punctiforme ATCC 29133

<220>

<221> CDS

<222> (5) .. (775)

<400> 131

gcgc	atg	cat	cta	gaa	atg	atc	cag	tta	gaa	caa	cca	ctc	agt	cat	caa	49
	Met	His	Leu	Glu	Met	Ile	Gln	Leu	Glu	Gln	Pro	Leu	Ser	His	Gln	
1					5				10						15	

gca	aaa	ctg	act	cca	gta	ctg	aga	agt	aaa	tct	cag	ttt	aag	ggg	ctt	97
Ala	Lys	Leu	Thr	Pro	Val	Leu	Arg	Ser	Lys	Ser	Gln	Phe	Lys	Gly	Leu	
				20					25					30		

ttc	att	gct	att	gtc	att	gtt	agc	gca	tgg	gtc	att	agc	ctg	agt	tta	145
Phe	Ile	Ala	Ile	Val	Ile	Val	Ser	Ala	Trp	Val	Ile	Ser	Leu	Ser	Leu	
			35					40					45			

tta	ctt	tcc	ctt	gac	atc	tca	aag	cta	aaa	ttt	tgg	atg	tta	ttg	cct	193
Leu	Leu	Ser	Leu	Asp	Ile	Ser	Lys	Leu	Lys	Phe	Trp	Met	Leu	Leu	Pro	
		50					55					60				

gtt	ata	cta	tgg	caa	aca	ttt	tta	tat	acg	gga	tta	ttt	att	aca	tct	241
Val	Ile	Leu	Trp	Gln	Thr	Phe	Leu	Tyr	Thr	Gly	Leu	Phe	Ile	Thr	Ser	
	65				70					75						

cat	gat	gcc	atg	cat	ggc	gta	gta	ttt	ccc	caa	aac	acc	aag	att	aat	289
His	Asp	Ala	Met	His	Gly	Val	Val	Phe	Pro	Gln	Asn	Thr	Lys	Ile	Asn	
80					85				90					95		

cat	ttg	att	gga	aca	ttg	acc	cta	tcc	ctt	tat	ggt	ctt	tta	cca	tat	337
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

His Leu Ile Gly Thr Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr	
100 105 110	
caa aaa cta ttg aaa aaa cat tgg tta cac cac cac aat cca gca agc	385
Gln Lys Leu Leu Lys Lys His Trp Leu His His His Asn Pro Ala Ser	
115 120 125	
tca ata gac ccg gat ttt cac aat ggt aaa cac caa agt ttc ttt gct	433
Ser Ile Asp Pro Asp Phe His Asn Gly Lys His Gln Ser Phe Phe Ala	
130 135 140	
tgg tat ttt cat ttt atg aaa ggt tac tgg agt tgg ggg caa ata att	481
Trp Tyr Phe His Phe Met Lys Gly Tyr Trp Ser Trp Gly Gln Ile Ile	
145 150 155	
gcg ttg act att att tat aac ttt gct aaa tac ata ctc cat atc cca	529
Ala Leu Thr Ile Ile Tyr Asn Phe Ala Lys Tyr Ile Leu His Ile Pro	
160 165 170 175	
agt gat aat cta act tac ttt tgg gtg cta ccc tcg ctt tta agt tca	577
Ser Asp Asn Leu Thr Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser	
180 185 190	
tta caa tta ttc tat ttt ggt act ttt tta ccc cat agt gaa cca ata	625
Leu Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile	
195 200 205	
ggg ggt tat gtt cag cct cat tgt gcc caa aca att agc cgt cct att	673
Gly Gly Tyr Val Gln Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile	
210 215 220	
tgg tgg tca ttt atc acg tgc tat cat ttt ggc tac cac gag gaa cat	721
Trp Trp Ser Phe Ile Thr Cys Tyr His Phe Gly Tyr His Glu Glu His	
225 230 235	
cac gaa tat cct cat att tct tgg tgg cag tta cca gaa att tac aaa	769
His Glu Tyr Pro His Ile Ser Trp Trp Gln Leu Pro Glu Ile Tyr Lys	
240 245 250 255	
gca aaa tagtctagag catgcgc	792
Ala Lys	

<210> 132

<211> 257

<212> PRT

<213> Nostoc punctiforme ATCC 29133

<400> 132

Met His Leu Glu Met Ile Gln Leu Glu Gln Pro Leu Ser His Gln Ala
1 5 10 15

Lys Leu Thr Pro Val Leu Arg Ser Lys Ser Gln Phe Lys Gly Leu Phe
20 25 30

Ile Ala Ile Val Ile Val Ser Ala Trp Val Ile Ser Leu Ser Leu Leu
 35 40 45

Leu Ser Leu Asp Ile Ser Lys Leu Lys Phe Trp Met Leu Leu Pro Val
 50 55 60

Ile Leu Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser His
 65 70 75 80

Asp Ala Met His Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn His
 85 90 95

Leu Ile Gly Thr Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr Gln
 100 105 110

Lys Leu Leu Lys Lys His Trp Leu His His His Asn Pro Ala Ser Ser
 115 120 125

Ile Asp Pro Asp Phe His Asn Gly Lys His Gln Ser Phe Phe Ala Trp
 130 135 140

Tyr Phe His Phe Met Lys Gly Tyr Trp Ser Trp Gly Gln Ile Ile Ala
 145 150 155 160

Leu Thr Ile Ile Tyr Asn Phe Ala Lys Tyr Ile Leu His Ile Pro Ser
 165 170 175

Asp Asn Leu Thr Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser Leu
 180 185 190

Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile Gly
 195 200 205

Gly Tyr Val Gln Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile Trp
 210 215 220

Trp Ser Phe Ile Thr Cys Tyr His Phe Gly Tyr His Glu Glu His His
 225 230 235 240

Glu Tyr Pro His Ile Ser Trp Trp Gln Leu Pro Glu Ile Tyr Lys Ala
 245 250 255

Lys

<210> 133

<211> 26

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 133

gtcgaccctg ctttaatgag atatgc

26

<210> 134

<211> 27

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 134

ctcgagcttg gacaatcagt aaattga

27

<210> 135

<211> 210

<212> DNA

<213> Agrobacterium tumefaciens

<220>

<221> Terminator

<400> 135

gtcgaccctg ctttaatgag atatgcgaga cgcctatgat cgcgatgat ttgctttcaa 60

ttctgttggtg cacgttgtaa aaaacctgag catgtgtagc tcagatcctt accgcgggtt 120

tcggttcatt ctaatgaata taccaccgt tactatcgta tttttatgaa taatattctc 180

cgttcaattt actgattgtc caagctcgag 210

<210> 136

<211> 37

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 136

cccgggaatt cttcattatt tcgattttga tttcgtg

37

<210> 137

<211> 38

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 137

aagcttggtt gatcagaaga agaagaagaa gatgaact

38

<210> 138

<211> 652

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> Promoter

<400> 138

cccgggaatt cttcattatt tcgattttga tttcgtgacc agcgaacgca gaataccttg 60

ttgtgtaata ctttaccctg gtaaatcaaa aacaaaaagg cttttgagct tttttagatt 120

gaatttctct ggctgatctt ttctgtacag attcatatat ctgcagagac gatattcattg 180

attatttgag cttcttttga actatttcgt gtaatttggg atgagagctc tatgtatgtg 240

tgtaaacctt gaagacaaca agaaaggtaa caagtggagg agggatgact ccatgtcaaa 300

atagatgtca taagaggccc atcaataagt gcttgagccc attagctagc ccagtaacta 360

ccagattgtg agatggatgt gtgaacagtt ttttttttga tgtaggactg aaatgtgaac 420

aacaggcgca tgaaaggcta aattaggaca atgataagca gaaataactt atcctctcta 480

acacttggcc tcacattgcc cttcacacaa tccacacaca tccaatcaca acctcatcat 540
 atatctcccg ctaatctttt tttctttgat cttttttttt ttgcttatta tttttttgac 600
 tttgatctcc catcagttca tcttcttctt cttcttctga tcaaccaagc tt 652

<210> 139

<211> 29

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 139

gagctctagc gcaatcttat gtggtacaa

29

<210> 140

<211> 29

<212> DNA

<<213> Artificial sequence

<220>

<223> Primer

<400> 140

aagcttttct tgaaagtaaa gattgagtc

29

<210> 141

<211> 1773

<212> DNA

<213> Petunia hybrida

<220>

<221> Promoter

<400> 141

gagctctagc gcaatcttat gtggtacaaa tcttgattag tcgggaaaaa atgatgtggc

60

cctacaaatg gttggaggat gggagatttg gctctatcta gagttatgtg gttgttgaag

120

catttggtta ctctctgctg tggtagttgg catatccaca ttgtctcctt ccacttttat

180

gacaattacg tgaaagttat gggttgtttt gtctattttt gtcgaggcct ttcttttcct 240
 tccagggttg tgaagatggg ccaattcgat tagaataatg ttttgagctt tagcatattc 300
 tctctcgttt acacgattat agtaataatg atataggatg acagaagttg acacataaat 360
 tttttattct ctccatttac tttaatccaa atctcaccta ccctaaactt ctttaatatg 420
 tattcaatag tctatccgag taaattgtaa atttaacaac cattgataat attgacacct 480
 actaacatat actagtaaag agaataattaa catggcacat ataatttgat gcaaaatgag 540
 tatgatgaaa tttaaaccce aaatctcttg attttgacag tgtcaccttg acttggttaac 600
 taataagtca tgtttttagtg gcagaaagac aaactcatcc accaactgta tagcaataaa 660
 aaatagaaga atcttcctga ggcaaagttt tggaaaaatt aagagtggct gagatttaat 720
 ttcaacagga attagttcca cttactttt aggttacgat acagtgctaa ttaaataact 780
 taattgtatt agatatttct tgcacctaaa aaatttaaaa actgaaaaaa ggtagcaatc 840
 aaaataaaca aaaggacaaa ataagtgaag ggtacagcca ccaaccctgg cggctcactg 900
 tttgttggtt aaaacgtaga cttacacctt ccaaaatcta caactaaaat gaggcaataa 960
 tactttgccc aaaattacca agaaaagaaa aagaaaggaa tcccttaata ttactctcct 1020
 ccatttcaca ataaatatcc tagtttgact taaattagag tttaaaaaat gaaagacgac 1080
 ttttaaaact tgtaatctaa aataaatcat agttaaatgt gtggctataa atcattgtat 1140

 taacggtaaa gtggttaagt taaaagttaa ttgttttcaa atataaaatt gtactatcat 1200
 tctttttgga atggactaat aagaaaacta tgacatccat tatggagcgg agggagtatc 1260
 tccttttaac aataaccttt gtcccttcaa ttcaattatc agtatgcaaa cattaaaaat 1320
 tattattgat gttaagtacc acatcatcct taatgataga atcatcgtag aacgcttttc 1380
 caggcacaca ttcaaactag ttagaccagt accacacatc gaatattcca gacttctttg 1440
 tttgaatagt cgactacatt ggataatgga acttctcgaa ttaacttoga attagtcgag 1500
 cccaaaataa tatatacgtc ggggtgaaaa ctataaaatg tttgacaaaa atgtcaaatt 1560
 aatatatcaa tctgcaacaa ccttttcacc ttgagaacac agctgaaatt ttttacaag 1620
 gtagttgggtg aagctagtca gcgaatccca ttaccttcca ctctacctaa ccccttcac 1680
 caacaacaaa tttctgtaat ttaaaaacta gccaaaaaag aactctcttt taaaaagagc 1740
 caaagactca atctttactt tcaagaaaag ctt 1773

<210> 142

<211> 39

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 142

gcgcatgcat ctagaaatga atttttgtga taaaccagt 39

<210> 143

<211> 37

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 143

gcgcatgctc tagattacga attgggttact gaattgt 37

<210> 144

<211> 819

<212> DNA

<213> Nostoc punctiforme ATCC 29133

<220>

<221> CDS

<222> (5)..(802)

<400> 144

gcgc atg cat cta gaa atg aat ttt tgt gat aaa cca gtt agc tat tat 49
Met His Leu Glu Met Asn Phe Cys Asp Lys Pro Val Ser Tyr Tyr
1 5 10 15

ggt gca ata gag caa tta agt gct aaa gaa gat act gtt tgg ggg ctg 97
Val Ala Ile Glu Gln Leu Ser Ala Lys Glu Asp Thr Val Trp Gly Leu
20 25 30

gtg att gtc ata gta att att agt ctt tgg gta gct agt ttg gct ttt 145
Val Ile Val Ile Val Ile Ile Ser Leu Trp Val Ala Ser Leu Ala Phe
35 40 45

tta cta gct att aat tat gcc aaa gtc cca att tgg ttg ata cct att 193
Leu Leu Ala Ile Asn Tyr Ala Lys Val Pro Ile Trp Leu Ile Pro Ile
50 55 60

gca ata gtt tgg caa atg ttc ctt tat aca ggg cta ttt att act gca	241
Ala Ile Val Trp Gln Met Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala	
65 70 75	
cat gat gct atg cat ggg tca gtt tat cgt aaa aat ccc aaa att aat	289
His Asp Ala Met His Gly Ser Val Tyr Arg Lys Asn Pro Lys Ile Asn	
80 85 90 95	
aat ttt atc ggt tca cta gct gta gcg ctt tac gct gtg ttt cca tat	337
Asn Phe Ile Gly Ser Leu Ala Val Ala Leu Tyr Ala Val Phe Pro Tyr	
100 105 110	
caa cag atg tta aag aat cat tgc tta cat cat cgt cat cct gct agc	385
Gln Gln Met Leu Lys Asn His Cys Leu His His Arg His Pro Ala Ser	
115 120 125	
gaa gtt gac cca gat ttt cat gat ggt aag aga aca aac gct att ttc	433
Glu Val Asp Pro Asp Phe His Asp Gly Lys Arg Thr Asn Ala Ile Phe	
130 135 140	
tgg tat ctc cat ttc atg ata gaa tac tcc agt tgg caa cag tta ata	481
Trp Tyr Leu His Phe Met Ile Glu Tyr Ser Ser Trp Gln Gln Leu Ile	
145 150 155	
gta cta act atc cta ttt aat tta gct aaa tac gtt ttg cac atc cat	529
Val Leu Thr Ile Leu Phe Asn Leu Ala Lys Tyr Val Leu His Ile His	
160 165 170 175	
caa ata aat ctc atc tta ttt tgg agt att cct cca att tta agt tcc	577
Gln Ile Asn Leu Ile Leu Phe Trp Ser Ile Pro Pro Ile Leu Ser Ser	
180 185 190	
att caa ctg ttt tat ttc gga aca ttt ttg cct cat cga gaa ccc aag	625
Ile Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Arg Glu Pro Lys	
195 200 205	
aaa gga tat gtt tat ccc cat tgc agc caa aca ata aaa ttg cca act	673
Lys Gly Tyr Val Tyr Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr	
210 215 220	
ttt ttg tca ttt atc gct tgc tac cac ttt ggt tat cat gaa gaa cat	721
Phe Leu Ser Phe Ile Ala Cys Tyr His Phe Gly Tyr His Glu Glu His	
225 230 235	
cat gag tat ccc cat gta cct tgg tgg caa ctt cca tct gta tat aag	769
His Glu Tyr Pro His Val Pro Trp Trp Gln Leu Pro Ser Val Tyr Lys	
240 245 250 255	
cag aga gta ttc aac aat tca gta acc aat tcg taatctagag catgcgc	819
Gln Arg Val Phe Asn Asn Ser Val Thr Asn Ser	
260 265	

<210> 145

<211> 266

<212> PRT

<213> Nostoc punctiforme ATCC 29133

<400> 145

Met His Leu Glu Met Asn Phe Cys Asp Lys Pro Val Ser Tyr Tyr Val
 1 5 10 15

Ala Ile Glu Gln Leu Ser Ala Lys Glu Asp Thr Val Trp Gly Leu Val
 20 25 30

Ile Val Ile Val Ile Ile Ser Leu Trp Val Ala Ser Leu Ala Phe Leu
 35 40 45

Leu Ala Ile Asn Tyr Ala Lys Val Pro Ile Trp Leu Ile Pro Ile Ala
 50 55 60

Ile Val Trp Gln Met Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His
 65 70 75 80

Asp Ala Met His Gly Ser Val Tyr Arg Lys Asn Pro Lys Ile Asn Asn
 85 90 95

Phe Ile Gly Ser Leu Ala Val Ala Leu Tyr Ala Val Phe Pro Tyr Gln
 100 105 110

Gln Met Leu Lys Asn His Cys Leu His His Arg His Pro Ala Ser Glu
 115 120 125

Val Asp Pro Asp Phe His Asp Gly Lys Arg Thr Asn Ala Ile Phe Trp
 130 135 140

Tyr Leu His Phe Met Ile Glu Tyr Ser Ser Trp Gln Gln Leu Ile Val
 145 150 155 160

Leu Thr Ile Leu Phe Asn Leu Ala Lys Tyr Val Leu His Ile His Gln
 165 170 175

Ile Asn Leu Ile Leu Phe Trp Ser Ile Pro Pro Ile Leu Ser Ser Ile
 180 185 190

Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Arg Glu Pro Lys Lys
 195 200 205

Gly Tyr Val Tyr Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr Phe
 210 215 220

Leu Ser Phe Ile Ala Cys Tyr His Phe Gly Tyr His Glu Glu His His

33

32

49

	Met	His	Leu	Glu	Met	Ala	Ile	Ala	Ile	Ser	Ile	Trp	Ala	Ile		
	1				5					10				15		
97	agc	cta	ggt	ttg	tta	ctt	tat	att	gat	ata	tcc	caa	ttc	aag	ttt	tgg
	Ser	Leu	Gly	Leu	Leu	Leu	Tyr	Ile	Asp	Ile	Ser	Gln	Phe	Lys	Phe	Trp
				20						25					30	
145	atg	ttg	tta	ccg	ctc	ata	ttt	tgg	caa	aca	ttt	tta	tat	acg	gga	tta
	Met	Leu	Leu	Pro	Leu	Ile	Phe	Trp	Gln	Thr	Phe	Leu	Tyr	Thr	Gly	Leu
				35					40					45		
193	ttt	att	aca	gct	cat	gat	gcc	atg	cat	ggg	gta	gtt	ttt	ccc	aaa	aat
	Phe	Ile	Thr	Ala	His	Asp	Ala	Met	His	Gly	Val	Val	Phe	Pro	Lys	Asn
			50					55					60			
241	ccc	aaa	atc	aac	cat	ttc	att	ggc	tca	ttg	tgc	ctg	ttt	ctt	tat	ggt
	Pro	Lys	Ile	Asn	His	Phe	Ile	Gly	Ser	Leu	Cys	Leu	Phe	Leu	Tyr	Gly
		65					70					75				
289	ctt	tta	cct	tat	caa	aaa	ctt	tta	aaa	aag	cat	tgg	cta	cat	cac	cat
	Leu	Leu	Pro	Tyr	Gln	Lys	Leu	Leu	Lys	Lys	His	Trp	Leu	His	His	His
	80					85					90					95
337	aat	cca	gcc	agt	gaa	aca	gat	cca	gat	ttt	cac	aac	ggg	aag	cag	aaa
	Asn	Pro	Ala	Ser	Glu	Thr	Asp	Pro	Asp	Phe	His	Asn	Gly	Lys	Gln	Lys
					100					105					110	
385	aac	ttt	ttt	gct	tgg	tat	tta	tat	ttt	atg	aag	cgt	tac	tgg	agt	tgg
	Asn	Phe	Phe	Ala	Trp	Tyr	Leu	Tyr	Phe	Met	Lys	Arg	Tyr	Trp	Ser	Trp
				115					120					125		
433	tta	caa	att	atc	aca	tta	atg	att	att	tat	aac	tta	cta	aaa	tat	ata
	Leu	Gln	Ile	Ile	Thr	Leu	Met	Ile	Ile	Tyr	Asn	Leu	Leu	Lys	Tyr	Ile
			130					135					140			
481	tgg	cat	ttt	cca	gag	gat	aat	atg	act	tat	ttt	tgg	gta	gtt	ccc	tca
	Trp	His	Phe	Pro	Glu	Asp	Asn	Met	Thr	Tyr	Phe	Trp	Val	Val	Pro	Ser
		145					150					155				
529	att	tta	agt	tct	tta	caa	tta	ttt	tat	ttt	gga	act	ttt	cta	ccc	cac
	Ile	Leu	Ser	Ser	Leu	Gln	Leu	Phe	Tyr	Phe	Gly	Thr	Phe	Leu	Pro	His
	160					165					170					175
577	agt	gag	cct	gta	gaa	ggt	tat	aaa	gag	cct	cat	cgt	tcc	caa	act	att
	Ser	Glu	Pro	Val	Glu	Gly	Tyr	Lys	Glu	Pro	His	Arg	Ser	Gln	Thr	Ile
				180						185					190	
625	agc	cgt	ccc	att	tgg	tgg	tca	ttt	ata	act	tgt	tac	cat	ttt	ggt	tat
	Ser	Arg	Pro	Ile	Trp	Trp	Ser	Phe	Ile	Thr	Cys	Tyr	His	Phe	Gly	Tyr
				195					200					205		
673	cat	tac	gaa	cat	cat	gaa	tac	ccc	cat	ggt	cct	tgg	tgg	caa	tta	cca
	His	Tyr	Glu	His	His	Glu	Tyr	Pro								

<210> 149

<211> 233

<212> PRT

<213> Nodularia spumigena NSOR10

<400> 149

Met His Leu Glu Met Ala Ile Ala Ile Ile Ser Ile Trp Ala Ile Ser
1 5 10 15

Leu Gly Leu Leu Leu Tyr Ile Asp Ile Ser Gln Phe Lys Phe Trp Met
20 25 30

Leu Leu Pro Leu Ile Phe Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe
35 40 45

Ile Thr Ala His Asp Ala Met His Gly Val Val Phe Pro Lys Asn Pro
50 55 60

Lys Ile Asn His Phe Ile Gly Ser Leu Cys Leu Phe Leu Tyr Gly Leu
65 70 75 80

Leu Pro Tyr Gln Lys Leu Leu Lys Lys His Trp Leu His His His Asn
85 90 95

Pro Ala Ser Glu Thr Asp Pro Asp Phe His Asn Gly Lys Gln Lys Asn
100 105 110

Phe Phe Ala Trp Tyr Leu Tyr Phe Met Lys Arg Tyr Trp Ser Trp Leu
115 120 125

Gln Ile Ile Thr Leu Met Ile Ile Tyr Asn Leu Leu Lys Tyr Ile Trp
130 135 140

His Phe Pro Glu Asp Asn Met Thr Tyr Phe Trp Val Val Pro Ser Ile
145 150 155 160

Leu Ser Ser Leu Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Ser
165 170 175

Glu Pro Val Glu Gly Tyr Lys Glu Pro His Arg Ser Gln Thr Ile Ser
180 185 190

Arg Pro Ile Trp Trp Ser Phe Ile Thr Cys Tyr His Phe Gly Tyr His
195 200 205

Tyr Glu His His Glu Tyr Pro His Val Pro Trp Trp Gln Leu Pro Glu
 210 215 220

Ile Tyr Lys Met Ser Lys Ser Asn Leu
 225 230

<210> 150

<211> 24

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 150
 gaattcctgc aatagaatgt tgag

24

<210> 151

<211> 25

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 151
 ctcgagctta cgagcatttt ctaag

25

<210> 152

<211> 25

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 152
 gaattcccaa taataatcta cagcc

25

<210> 153

<211> 25

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 153

aagcttgac gagcctctct ctatt

25

<210> 154

<211> 25

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 154

gtcgacctct ccattttttc ttcaa

25

<210> 155

<211> 22

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 155

gaattcggca cgagcctctc tc

22

<210> 156

<211> 23

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 156

ggatcctctc cattttttct tca

23

<210> 157

<211> 24

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 157

gagctctagc gcaatcttat gtgg

24

<210> 158

<211> 22

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 158

ccatggttct cacttctgta tg

22

<210> 159

<211> 25

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 159

aagcttccat ggcggccgga atttc

25

<210> 160

<211> 307

<212> DNA

<213> Vicia faba

<220>

<221> Terminator

<400> 160

gaattcctgc aatagaatgt tgagggtgacc acttttctgta ataaaataat tataaaataa	60
attdagaatt gctgtagtca agaacatcag ttctaaaata ttaataaagt tatggccttt	120
tgacatatgt gtttcgataa aaaaatcaaa ataaattgag atttattcga aatacaatga	180
aagtttgcag atatgagata tgtttctaca aaataataac ttaaaaactca actatatgct	240
aatgtttttc ttggtgtgtt tcatagaaaa ttgtatccgt ttcttagaaa atgctcgtaa	300
gctcgag	307

<210> 161

<211> 1020

<212> DNA

<213> Lycopersicon esculentum

<220>

<221> misc_feature

<223> Nucleic acid encoding a beta-hydroxylase

<400> 161

aagcttccat ggcggccgga atttcagcct ccgctagttc ccgaaccatt cgcctccgtc	60
ataaccggtt tctcagtcca aaatccgcct caaccgcccc gccggttctg ttcttctctc	120
cgttaactcg caatdddggc gcaatdddgc tgtctagaag aaagccgaga ttggcggttt	180
gttttgtgct ggagaatgag aaattgaata gtactatcga aagtgagagt gaagtaatag	240
aggatcggat acaagtagag attaatgagg agaagagttt agctgccagt tggctggcgg	300
agaaattggc gaggaagaaa tcggagaggt ttacttatct tgtggcagct gtgatgtcta	360
gtttggggat tacttctatg gcgattttgg cggtttatta cagatdddca tggcaaatgg	420
agggtggaga agtgccdttdt tctgaaatgt tagctacatt cactctctcg tttggcgctg	480
ccgtaggaat ggagtactgg gcgagatggg ctcatagagc actatggcat gcttcttdat	540
ggcacatgca cgagtcgcac catagaccaa gagaaggacc ttttgagatg aacgacgttd	600
tcgccataac aaatgctgtt ccagctatag gtcttcttdt ctacggtdtdt ttccataaag	660
ggatcgtccc tggcctctgt ttcggcgctg gattggggat cacagtattd gggatggctt	720
acatgttcgt tcacgatgga ctggttcata agagattdtc cgtagggcct attgccaacg	780
tgcttactt tcggagggtg gctgcagcac atcagcttda tctctcgac aaattdgatg	840

gtgtcccata tggcttgttt ctaggaccta aggaattgga agaagtagga ggacttgaag 900
 agttagaaaa ggaagtcaac cgaaggatta aaattttctaa gggattatta tgatcaaaaag 960
 atacgtctga taataataaa atgcgattgt atttaggctg tagattatta ttgggaattc 1020

<210> 162

<211> 1802

<212> DNA

<213> Petunia hybrida

<220>

<221> Promoter

<400> 162

gagctctagc gcaatcttat gtggtacaaa tcttgattag tcgggaaaaa atgatgtggc 60
 cctacaaatg gttggaggat gggagatttg gctctatcta gagttatgtg gttgttgaag 120
 catttggtta ctctctgctg tggtagttgg catatccaca ttgtctcctt ccacttttat 180
 gacaattacg tgaaagttat gggttgtttt gtctattttt gtcgaggcct ttcttttctt 240
 tccaggttgt tgaagatggg ccaattcgat tagaataatg ttttgagctt tagcatattc 300
 tctctcgttt acacgattat agtaataatg atataggatg acagaagttg acacataaat 360
 tttttattct ctccatttac tttaatccaa atctcaccta ccctaaactt ctttaatatg 420
 tattcaatag tctatccgag taaattgtaa atttaacaac cattgataat attgacacct 480
 actaacatat actagtaaag agaataattaa catggcacat ataatttgat gcaaaatgag 540
 tatgatgaaa tttaaaccca aaatctcttg attttgacag tgtcaccttg acttgttaac 600
 taataagtca tgttttagtg gcagaaagac aaactcatcc accaactgta tagcaataaa 660
 aaatagaaga atcttctctga ggcaaagttt tggaaaaatt aagagtggct gagatttaat 720
 ttcaacagga attagttcca cttaactttt aggttacgat acagtgctaa ttaaataact 780
 taattgtatt agatatttct tgcacctaaa aaatttaaaa actgaaaaaa ggtagcaatc 840
 aaaataaaca aaaggacaaa ataagtgaaa ggtacagcca ccaaccctgg cggctcactg 900
 tttgttggtt aaaacgtaga cttacaccta ccaaaatcta caactaaaat gaggcaataa 960
 tactttgccc aaaattacca agaaaagaaa aagaaaggaa tcccttaata ttactctcct 1020
 ccatttcaca ataaatatcc tagtttgact taaattagag tttaaaaaat gaaagacgac 1080
 ttttaaaaact tgtaatctaa aataaatcat agttaaatgt gtggctataa atcattgtat 1140

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taacggtaaa gtggtaagtt taaaagttaa ttgttttcaa atataaaatt gtactatcat 1200
tcttttttggga atggactaat aagaaaaacta tgacatccat tatggagcgg agggagtatc 1260
tcctttttaac aataaccttt gtcccttcaa ttcaattatc agtatgcaaa cattaaaaat 1320
tattattgat gttaagtacc acatcatcct taatgataga atcatcgtag aacgcttttc 1380
caggcacaca ttcaaactag ttagaccagt accacacatc gaatattcca gacttctttg 1440
tttgaatagt cgactacatt ggataatgga acttctcgaa ttaacttcga attagtcgag 1500
cccaaaataa tatatacgtc ggggtggaaaa ctataaaatg tttgacaaaa atgtcaaatt 1560
aatatatcaa tctgcaacaa ccttttcacc ttgagaacac agctgaaatt ttttacaaag 1620
gtagttggtg aagctagtca gcgaatccca ttaccttcca ctctacctaa ccccttcac 1680
caacaacaaa tttctgtaat ttaaaaaacta gccaaaaaag aactctcttt taaaaagagc 1740
caaagactca atctttactt tcaagaaaag ctttgcaatt catacagaag tgagaaccat 1800
gg 1802

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<210> 163

<211> 332

<212> DNA

<213> *Tagetes erecta*

<220>

<221> misc_feature

<223> beta-Hydroxylase sense fragment

<400> 163

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aagcttgcac gagcctctct ctattttttac acttcaatgg cggcagcaat tgctgtccct 60
tgtagctcaa gaccatttgg cttaggtcga atgcggttac ttggtcataa acccacaacc 120
ataacttgtc acttccccct ttctttttct atcaaatcat ttaccccaat tgttaggggc 180
agaagatgta ctgtttgttt tgttgccggt ggcgacagta atagtaacag taataataat 240
agtgacagta atagtaataa tccgggtctg gatttaaacc cggcgggttat gaaccgtaac 300
cgtttggttg aagaaaaaat ggagaggtcg ac 332

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<210> 164

<211> 332

<212> DNA

<213> Tagetes erecta

<220>

<221> misc_feature

<223> beta-Hydroxylase antisense fragment

<400> 164

gaattcggca cgagcctctc tctattttta cacttcaatg gcggcagcaa ttgctgtccc 60

ttgtagctca agaccatttg gcttaggtcg aatgcgggta cttgggcata aaccacaac 120

cataacttgt cacttccctt tttctttttc tatcaaatca tttaccccaa ttgttagggg 180

cagaagatgt actgtttgtt ttgttgccgg tggcgacagt aatagtaaca gtaataataa 240

tagtgacagt aatagtaata atccgggtct ggatttaaac ccggcggtta tgaaccgtaa 300

ccgtttgggt gaagaaaaaa tggagaggat cc 332

<210> 165

<211> 996

<212> DNA

<213> Unknown

<220>

<221> misc_feature

<222> (1)..(996)

<223> Artificial sequence

<400> 165

ggcacgagcc tctctctatt tttacacttc aatggcggca gcaattgctg tccctttag 60

ctcaagacca tttggcttag gtcgaatgcg gttacttggc cataaacca caaccataac 120

ttgtcacttc cccttttctt tttctatcaa atcatttacc ccaattgtta ggggcagaag 180

atgtactgtt tgttttgttg ccggtggcga cagtaatagt aacagtaata ataatagtga 240

cagtaatagt aataatccgg gtctggattt aaaccggcg gttatgaacc gtaaccgttt 300

ggttgaagaa aaaatggaga ggaaaaaatc ggaacgattt acttatcttg ttgcagctat 360

tatgtctact tttggaatta cttcaatggc gggtatggcg gtttattacc ggttttcatg 420

gcaaattggag ggtggagaaa ttccttatgt ggagatgttt ggtacatttg ctctctccgt 480

tggtgctgcg gtaggaatgg agtattgggc aagatgggct catgaggcac tatggcatgc 540
 ttctttgtgg cacatgcatg agtcacacca taagccacga gaagggtccgt ttgagcttaa 600
 tgatgtgttt gctataacaa atgcgggtccc ggccattgcg ttgcttagtt atgggttttt 660
 ccacaaaggc ataattccgg gtctttgttt tggggcgggga ctgggaatta cgggtgtttgg 720
 aatggcgat atgttcgtcc acgacgggct agttcacaga agattccaag tgggtccgat 780
 tgcgaatgtt ccctatcttc gaagggttgc agcgggtcat cagctgcatc acacggaaaa 840
 atttaatggt gttccttatg gcttgttctt gggacctaa gagctagaag aagtgggtgg 900
 tacggaagaa ttggacaagg agattcaaag aagaattaaa ttgtataata atactaaata 960
 aataaatttt gtataaaatt aatataattt aatgat 996

<210> 166

<211> 19

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 166

tgcaaaagta actctttat

19

<210> 167

<211> 19

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 167

aggtgcatga ccaagtaac

19

<210> 168

<211> 1033

<212> DNA

<213> *Arabidopsis thaliana*

<220>

<221> Promoter

<223> P76

<400> 168

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agggtgcatga ccaagtaaca atttgattcc tttccagcat aacgtcatgt tggttgcaaa      60
aagaaggcaa agtagagcaa gcaagcaagc aaagcatttt tcttatttta tattttgttg      120
cggattccac caccacttg aaaaattgac atgtcacaat gatttcgtat cctagtcttt      180
tattatttaa cactctcaca atcccattac tctacacctc tttcattaag tcaacacacg      240
gttttcaaaa atccactacc ctcccaccac ctagaatctt ttgttaccta ccaacaccct      300
cctttgttct ctttatatat tgggtccaact aaatcaataa gggaaagcat ccttttggtt      360
ggaggaattg ctttcattct cactctttgt gtgttgatca atggactagc taataacaag      420
ttctcctct atatatattca aaagaatgga acagaaacat aaacgaaaga cagagtacct      480
gatgttgatg attcattgtc tgtctggagc tcccaaatgc cttttatgct tacatattca      540
taaccaacaa cggctattaa ttataaacca aaaacacgaa ataagtttgt agcaaagtga      600
aattaggaat cttggagatg gatccattag tagtaggata ataggatatg atggaatttg      660
gttggggaac agtgataact tacgcttgct tccggcgccg ggaaagttag aaaacctaca      720
aagtacagaa atggatctgg gccttgaagt gggcttttta ttaaagaaaa aaatacatct      780
ccgttatcaa tcaccatctt cttctatcta caaattaaag aaggtaacaa cagaacgtgg      840
tggatcatgt ggtaggcat taattatttg ctttgtttcg ccgttttggt aacacacaga      900
cacagttccg gtaagagctt ttgcagccac tctttatagt tatttagaat tggcgatcga      960

atcaatctca ctccctccct cccttaagtc ttgttgaatc tgctgaattg ttttataaag    1020
agttactttg gca                                                         1033

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<210> 169

<211> 18

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 169
atggaagctc ttctcaag

18

<210> 170

<211> 18

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 170
accttaccta aaacattt

18

<210> 171

<211> 1666

<212> DNA

<213> Lycopersicon esculentum

<220>

<221> CDS

<222> (1)..(1494)

<400> 171
atg gaa gct ctt ctc aag cct ttt cca tct ctt tta ctt tcc tct cct 48
Met Glu Ala Leu Leu Lys Pro Phe Pro Ser Leu Leu Leu Ser Ser Pro
1 5 10 15

aca ccc cat agg tct att ttc caa caa aat ccc tct ttt cta agt ccc 96
Thr Pro His Arg Ser Ile Phe Gln Gln Asn Pro Ser Phe Leu Ser Pro
20 25 30

acc acc aaa aaa aaa tca aga aaa tgt ctt ctt aga aac aaa agt agt 144
Thr Thr Lys Lys Lys Ser Arg Lys Cys Leu Leu Arg Asn Lys Ser Ser
35 40 45

aaa ctt ttt tgt agc ttt ctt gat tta gca ccc aca tca aag cca gag 192
Lys Leu Phe Cys Ser Phe Leu Asp Leu Ala Pro Thr Ser Lys Pro Glu
50 55 60

tct tta gat gtt aac atc tca tgg gtt gat cct aat tcg aat cgg gct 240
Ser Leu Asp Val Asn Ile Ser Trp Val Asp Pro Asn Ser Asn Arg Ala
65 70 75 80

caa ttc gac gtg atc att atc gga gct ggc cct gct ggg ctc agg cta 288
Gln Phe Asp Val Ile Ile Ile Gly Ala Gly Pro Ala Gly Leu Arg Leu
85 90 95

gct gaa caa gtt tct aaa tat ggt att aag gta tgt tgt gtt gac cct 336

Ala	Glu	Gln	Val	Ser	Lys	Tyr	Gly	Ile	Lys	Val	Cys	Cys	Val	Asp	Pro		
			100					105					110				
tca	cca	ctc	tcc	atg	tgg	cca	aat	aat	tat	ggg	gtt	tgg	gtt	gat	gag	384	
Ser	Pro	Leu	Ser	Met	Trp	Pro	Asn	Asn	Tyr	Gly	Val	Trp	Val	Asp	Glu		
		115					120					125					
ttt	gag	aat	tta	gga	ctg	gaa	aat	tgt	tta	gat	cat	aaa	tgg	cct	atg	432	
Phe	Glu	Asn	Leu	Gly	Leu	Glu	Asn	Cys	Leu	Asp	His	Lys	Trp	Pro	Met		
	130					135					140						
act	tgt	gtg	cat	ata	aat	gat	aac	aaa	act	aag	tat	ttg	gga	aga	cca	480	
Thr	Cys	Val	His	Ile	Asn	Asp	Asn	Lys	Thr	Lys	Tyr	Leu	Gly	Arg	Pro		
145					150					155					160		
tat	ggg	aga	gtt	agt	aga	aag	aag	ctg	aag	ttg	aaa	ttg	ttg	aat	agt	528	
Tyr	Gly	Arg	Val	Ser	Arg	Lys	Lys	Leu	Lys	Leu	Lys	Leu	Leu	Asn	Ser		
				165					170					175			
tgt	gtt	gag	aac	aga	gtg	aag	ttt	tat	aaa	gct	aag	gtt	tgg	aaa	gtg	576	
Cys	Val	Glu	Asn	Arg	Val	Lys	Phe	Tyr	Lys	Ala	Lys	Val	Trp	Lys	Val		
			180					185					190				
gaa	cat	gaa	gaa	ttt	gag	tct	tca	att	gtt	tgt	gat	gat	ggg	aag	aag	624	
Glu	His	Glu	Glu	Phe	Glu	Ser	Ser	Ile	Val	Cys	Asp	Asp	Gly	Lys	Lys		
		195					200					205					
ata	aga	ggg	agt	ttg	gtt	gtg	gat	gca	agt	ggg	ttt	gct	agt	gat	ttt	672	
Ile	Arg	Gly	Ser	Leu	Val	Val	Asp	Ala	Ser	Gly	Phe	Ala	Ser	Asp	Phe		
	210					215					220						
ata	gag	tat	gac	agg	cca	aga	aac	cat	ggg	tat	caa	att	gct	cat	ggg	720	
Ile	Glu	Tyr	Asp	Arg	Pro	Arg	Asn	His	Gly	Tyr	Gln	Ile	Ala	His	Gly		
225					230				235					240			
gtt	tta	gta	gaa	gtt	gat	aat	cat	cca	ttt	gat	ttg	gat	aaa	atg	gtg	768	
Val	Leu	Val	Glu	Val	Asp	Asn	His	Pro	Phe	Asp	Leu	Asp	Lys	Met	Val		
			245					250					255				
ctt	atg	gat	tgg	agg	gat	tct	cat	ttg	ggg	aat	gag	cca	tat	tta	agg	816	
Leu	Met	Asp	Trp	Arg	Asp	Ser	His	Leu	Gly	Asn	Glu	Pro	Tyr	Leu	Arg		
			260					265					270				
gtg	aat	aat	gct	aaa	gaa	cca	aca	ttc	ttg	tat	gca	atg	cca	ttt	gat	864	
Val	Asn	Asn	Ala	Lys	Glu	Pro	Thr	Phe	Leu	Tyr	Ala	Met	Pro	Phe	Asp		
		275					280					285					
aga	gat	ttg	gtt	ttc	ttg	gaa	gag	act	tct	ttg	gtg	agt	cgt	cct	gtt	912	
Arg	Asp	Leu	Val	Phe	Leu	Glu	Glu	Thr	Ser	Leu	Val	Ser	Arg	Pro	Val		
	290					295					300						
tta	tcg	tat	atg	gaa	gta	aaa	aga	agg	atg	gtg	gca	aga	tta	agg	cat	960	
Leu	Ser	Tyr	Met	Glu	Val	Lys	Arg	Arg	Met	Val	Ala	Arg	Leu	Arg	His		
305					310					315				320			
ttg	ggg	atc	aaa	gtg	aaa	agt	gtt	att	gag	gaa	gag	aaa	tgt	gtg	atc	1008	
Leu	Gly	Ile	Lys	Val	Lys	Ser	Val	Ile	Glu	Glu	Glu	Lys	Cys	Val	Ile		
			325					330					335				
cct	atg	gga	gga	cca	ctt	ccg	cgg	att	cct	caa	aat	gtt	atg	gct	att	1056	

Pro Met Gly Gly Pro Leu Pro Arg Ile Pro Gln Asn Val Met Ala Ile	
340 345 350	
ggt ggg aat tca ggg ata gtt cat cca tca aca ggg tac atg gtg gct	1104
Gly Gly Asn Ser Gly Ile Val His Pro Ser Thr Gly Tyr Met Val Ala	
355 360 365	
agg agc atg gct tta gca cca gta cta gct gaa gcc atc gtc gag ggg	1152
Arg Ser Met Ala Leu Ala Pro Val Leu Ala Glu Ala Ile Val Glu Gly	
370 375 380	
ctt ggc tca aca aga atg ata aga ggg tct caa ctt tac cat aga gtt	1200
Leu Gly Ser Thr Arg Met Ile Arg Gly Ser Gln Leu Tyr His Arg Val	
385 390 395 400	
tgg aat ggt ttg tgg cct ttg gat aga aga tgt gtt aga gaa tgt tat	1248
Trp Asn Gly Leu Trp Pro Leu Asp Arg Arg Cys Val Arg Glu Cys Tyr	
405 410 415	
tca ttt ggg atg gag aca ttg ttg aag ctt gat ttg aaa ggg act agg	1296
Ser Phe Gly Met Glu Thr Leu Leu Lys Leu Asp Leu Lys Gly Thr Arg	
420 425 430	
aga ttg ttt gac gct ttc ttt gat ctt gat cct aaa tac tgg caa ggg	1344
Arg Leu Phe Asp Ala Phe Phe Asp Leu Asp Pro Lys Tyr Trp Gln Gly	
435 440 445	
ttc ctt tct tca aga ttg tct gtc aaa gaa ctt ggt tta ctc agc ttg	1392
Phe Leu Ser Ser Arg Leu Ser Val Lys Glu Leu Gly Leu Leu Ser Leu	
450 455 460	
tgt ctt ttc gga cat ggc tca aac atg act agg ttg gat att gtt aca	1440
Cys Leu Phe Gly His Gly Ser Asn Met Thr Arg Leu Asp Ile Val Thr	
465 470 475 480	
aaa tgt cct ctt cct ttg gtt aga ctg att ggc aat cta gca ata gag	1488
Lys Cys Pro Leu Pro Leu Val Arg Leu Ile Gly Asn Leu Ala Ile Glu	
485 490 495	
agc ctt tgaatgtgaa aagtttgaat cattttcttc attttaattt ctttgattat	1544
Ser Leu	
tttcatatatt tctcaattgc aaaagtgaga taagagctac atactgtcaa caaataaact	1604
actattggaa agttaaaata tgtgtttggt gtatgttatt ctaatggaat ggattttgta	1664
aa	1666

<210> 172

<211> 498

<212> PRT

<213> Lycopersicon esculentum

<400> 172

Met Glu Ala Leu Leu Lys Pro Phe Pro Ser Leu Leu Leu Ser Ser Pro
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 Thr Pro His Arg Ser Ile Phe Gln Gln Asn Pro Ser Phe Leu Ser Pro
 20 25 30
 Thr Thr Lys Lys Lys Ser Arg Lys Cys Leu Leu Arg Asn Lys Ser Ser
 35 40 45
 Lys Leu Phe Cys Ser Phe Leu Asp Leu Ala Pro Thr Ser Lys Pro Glu
 50 55 60
 Ser Leu Asp Val Asn Ile Ser Trp Val Asp Pro Asn Ser Asn Arg Ala
 65 70 75 80
 Gln Phe Asp Val Ile Ile Ile Gly Ala Gly Pro Ala Gly Leu Arg Leu
 85 90 95
 Ala Glu Gln Val Ser Lys Tyr Gly Ile Lys Val Cys Cys Val Asp Pro
 100 105 110
 Ser Pro Leu Ser Met Trp Pro Asn Asn Tyr Gly Val Trp Val Asp Glu
 115 120 125
 Phe Glu Asn Leu Gly Leu Glu Asn Cys Leu Asp His Lys Trp Pro Met
 130 135 140
 Thr Cys Val His Ile Asn Asp Asn Lys Thr Lys Tyr Leu Gly Arg Pro
 145 150 155 160
 Tyr Gly Arg Val Ser Arg Lys Lys Leu Lys Leu Lys Leu Leu Asn Ser
 165 170 175
 Cys Val Glu Asn Arg Val Lys Phe Tyr Lys Ala Lys Val Trp Lys Val
 180 185 190
 Glu His Glu Glu Phe Glu Ser Ser Ile Val Cys Asp Asp Gly Lys Lys
 195 200 205
 Ile Arg Gly Ser Leu Val Val Asp Ala Ser Gly Phe Ala Ser Asp Phe
 210 215 220
 Ile Glu Tyr Asp Arg Pro Arg Asn His Gly Tyr Gln Ile Ala His Gly
 225 230 235 240

Val Leu Val Glu Val Asp Asn His Pro Phe Asp Leu Asp Lys Met Val
245 250 255

Leu Met Asp Trp Arg Asp Ser His Leu Gly Asn Glu Pro Tyr Leu Arg
260 265 270

Val Asn Asn Ala Lys Glu Pro Thr Phe Leu Tyr Ala Met Pro Phe Asp
275 280 285

Arg Asp Leu Val Phe Leu Glu Glu Thr Ser Leu Val Ser Arg Pro Val
290 295 300

Leu Ser Tyr Met Glu Val Lys Arg Arg Met Val Ala Arg Leu Arg His
305 310 315 320

Leu Gly Ile Lys Val Lys Ser Val Ile Glu Glu Glu Lys Cys Val Ile
325 330 335

Pro Met Gly Gly Pro Leu Pro Arg Ile Pro Gln Asn Val Met Ala Ile
340 345 350

Gly Gly Asn Ser Gly Ile Val His Pro Ser Thr Gly Tyr Met Val Ala
355 360 365

Arg Ser Met Ala Leu Ala Pro Val Leu Ala Glu Ala Ile Val Glu Gly
370 375 380

Leu Gly Ser Thr Arg Met Ile Arg Gly Ser Gln Leu Tyr His Arg Val
385 390 395 400

Trp Asn Gly Leu Trp Pro Leu Asp Arg Arg Cys Val Arg Glu Cys Tyr
405 410 415

Ser Phe Gly Met Glu Thr Leu Leu Lys Leu Asp Leu Lys Gly Thr Arg
420 425 430

Arg Leu Phe Asp Ala Phe Phe Asp Leu Asp Pro Lys Tyr Trp Gln Gly
435 440 445

Phe Leu Ser Ser Arg Leu Ser Val Lys Glu Leu Gly Leu Leu Ser Leu
450 455 460

Cys Leu Phe Gly His Gly Ser Asn Met Thr Arg Leu Asp Ile Val Thr
465 470 475 480

Lys	Cys	Pro	Leu	Pro	Leu	Val	Arg	Leu	Ile	Gly	Asn	Leu	Ala	Ile	Glu
			485						490					495	

Ser Leu